STIC-Biotech/ChemLib

From:

Snedden, Sheridan

Sent:

Monday, February 03, 2003 7:29 PM STIC-Biotech/ChemLib

To: Subject:

Sequence Search 09701463

Sheridan SNEDDEN ID# 79298 Date: 2/3 /2002

AU 1653 308-4843

Serial #: 09701463 Room Location: 10A12

Mail Box: 9B01

1). Search for SEQ ID NO: 1

Please **DO NOT SEARCH** the PENDING PATENTS Database.

Thanks, Examiner Snedden #79298 A.U. 1653/9B01 Office Location: 10A12 Phone #: 305-4843

Edward Hart Technica Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

Searcher:
Phone:
Location:/
Date Picked Up: 7/4/03
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:/
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (w	here applic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:_	02
WWW/Internet:	_
Other (specify):	

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BioTech-Chem Library Search Results Feedback Form (Optional)



The search results generated for your recent request are attached. If you have any questions or commer (compliments or complaints) about the scope or the results of the search, please contact the RioTech-C searcher who conducted the search or contact:

Mary Hale, Supervisor, 308-4. CM-1 Room 1E01

	I am an examiner in Workgroup: (Example: 1610)
>	Relevant prior art found, search results used as follows:
	102 rejection
	103 rejection
	☐ Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
۶	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Search results were not useful in determining patentability or understanding the invent

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or mary.hale@uspto.gov

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GenCore version 5.1.3 Compugen Ltd.

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Database
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SUMMARIES

Result		Query) 1	3	=	
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1	1504		276	21	AAY49442	Human plasma Zn-al
2	910	60.5	170	21	AAB43862	Human cancer assoc
ω	800.5	53.2	183	22	AAB80275	Human prostate can
4	791	52.6	171	20	AAY07773	Human secreted pro
₅	525	34.9	274	9	AAP80911	Consensus sequence
6	511	34.0	365	21	AAY68268	Human leukocyte an
7	511	34.0	365	21	AAY52922	HLA-A2/A28 family
8	511	34.0	365	22	AAB58683	HLA-A2/A28 protein
9	510	33.9	93	22	ABB39399	Peptide #6905 enco
10	510	33.9	93	22	ABB24181	Protein #6180 enco

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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AAB58689	AAY52928	AAY68274	AAB58690	AAY52929	AAY68275	AAY07033	AAP70590	AAB58686	AAB58680	AAY52925	AAY52919	AAY68271	AAY68265	AAP70155	AAB58691	AAY52930	AAY68276	AAB58687	AAY52926	AAY68272	AAB58684	AAY52923	AAY68269	AAB58685	AAB58681	AAY52924	AAY52920	AAY68270	AAY68266	AAU32882	ABG42512	AAM32919	AAM72688	AAM60079
HLA-A2/A28 protein	HLA-A2/A28 family	Human leukocyte an		HLA-A2/A28 family	Human leukocyte an	Breast cancer asso	Sequence of the hu	HLA-A2/A28 protein			HLA-A2/A28 family	leuko	Human leukocyte an		HLA-A2/A28 protein	HLA-A2/A28 family	Human leukocyte an		HLA-A2/A28 family	Human leukocyte an		HLA-A2/A28 family	0				HLA-A2/A28 family	leukocyte	leukocyte a		Human peptide enco	de #69	bone n	Human brain expres

ALIGNMENTS

RESULT 1 AAY49442 17-MAR-2000 AAY49442; AAY49442 standard; protein; 276 AA Human plasma Zn-alpha2-glycoprotein. (first entry)

Lipid mobilizing agent; zinc alpha2-glycoprotein; adenylate cyclase; fat metabolism; muscle synthesis; obesity; type II diabetes; body weight; muscle development; cachexia-inducing tumor; lipolysis; anticachectic; antitumor; cancer; human.

Homo sapiens.

WO9962939-A2

09-DEC-1999

01-JUN-1999; 99WO-GB01509

29-MAY-1998; 98GB-0011465

(TISD/) TISDALE M J. (TODO/) TODOROV P T.

Tisdale MJ, Todorov PT;

WPI; 2000-072831/06.

New lipid mobilizing agent used for treating obesity, and as diagnostic

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RESULT 2
AAB43862
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Matches 276
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                                                                          Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haematopolytic; cardiovascular disorder; infection; haematopolytic; cardiovascular disorder; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB43862 standard; Protein; 170 AA
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Homo sapiens
                                                  neurological
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DЬ Qy Dр οy Вþ

anticonvulsant;

Immunosuppressive;

ve; nootropic; r
antibacterial;

neuroprotective; antiviral;

antifungal;

antiparasitic;

vulnerary;
cardiant;

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nontropic; vasotropic; antipsoriatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating of ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activation or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease a bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 AAC78457 and AAB4420 represent sequences used in the exemplification cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antitheumatic; antiarthritic; antiviral; antiinflammatory; antityroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in AAB43398 to AAB44239. The proteins can have activities tissues and cells the genes are expressed in. Example of \varepsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200055350-A1
                                               Human prostate cancer antigen
                                                                                                                AAB80275;
                                                                                                                                                 AAB80275 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC77607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-2000;
                                                                                  24-APR-2001
                                                                                                                                                                                                                                 126
                                                                                                                                                                                                                                                                232
                                                                                                                                                                                                                                                                                                                               172
                                                                                                                                                                                                                                                                                                                                                                                                112
                                                                                                                                                                                                                                                                                                66
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                               σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention.
                                                                                                                                                                                                                                                                                                                                                                               FWKYYYDGKDYIEFNKEIPAWVPEDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKY 171
                                                                                                                                                                                                                                                              VLHNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                LKYSKNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGQVQEPELRGD 231
                                                                                                                                                                                                                                                                                                                                                               FWKYYYDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKY 65
                                                                                                                                                                                                                                 VLHNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                               {\tt LKYSKNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGEVQEPELRGD}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Page 1954; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                164; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC78071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to AAC78448 encode the human cancer associated proteins 398 to AAB44239. The proteins can have activities based o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US05882
                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENOME
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                                                                                                                                                 Protein;
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                                                                                entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                60.5%;
99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acids comprising sequences encoding peptides
                                                                                                                                                  183
                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 910; DB 21;
Pred. No. 1.1e-71;
                                                 #
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activities
                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activating
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on the
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 밁
                                                                                                                                                                                                                                                                                                                       The coding sequences and proteins of the present invention are useful for CC preventing, treating or ameliorating a medical condition; and for the CC diagnosis and treatment of diseases and disorders. Diseases and disorders CC that can be diagnosed and treated include (auto)immune diseases (e.g. CC graft versus host disease and rheumatoid arthritis), inflammatory and CC allergic disorders (e.g. asthma), hyperproliferative disorders (e.g. CC cancers and leukemias), cardiovascular disorders (e.g. heart attacks and CC arrythmias), cerebrovascular disorders (e.g. stroke), arterial occlusive CC disorders (e.g. arteriosclerosis), angliogenesis related disorders (e.g. cetinopathy and keloid scares), ocular disorders (e.g. glaucoma), CC neurological disorders (e.g. Alzheimer's, Parkinson's disease, epilepsy CC and Creutzfeld-Jakob disease) and infections caused by bacteria, fungi, CC viruses or parasites. They may also be useful for wound healing, CC regeneration, birth control and as a food additive or preservative.
                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1999;
13-AUG-1999;
17-AUG-1999;
06-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune disorder; cardiovascular disorder; neurological disease; infection; cancer; cytostatic; antiarthritic; antirheumatic; antiasthmatic; anticonvulsant; vasotropic; vulnerary; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid antigens, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01 - FEB - 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted protein; prostate cancer antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-2000;
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                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ROSE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ( HUMA - )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUL-2000;
                               179
 161
                                                          141
                                                                                                                    81
                                                                                                                                                61
                                                                                                                                                                             21
                                                                                                                                                                        present invention relates to humaing sequences (AAF72741-AAF72789)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-138554/14.
DB; AAF72743.
                          LDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGQVQEPELRGDVLHNGNG
                                                            GKDYIEFNKEIPAWVPFDPA
                                                                                     GKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYSKNI
                                                                                                                 EDWKQDSQLQKAREDIFMETLKDIVEYYNDSNGSHVLQGRFGCEIENNRSSGAFWKYYYD
                                                                                                                                              EDWKEDSQLQKARED - - METLKDIVEYYNDSNGSHVLQGRFGCEIENNRSSGAFWKYYYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
ROSEN
                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pages 385-386; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birse
                                                                                                                                                                                                                                                                                                183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0144972.
99US-0148681.
99US-0149173.
99US-0158004.
2000US-0194689.
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US19666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENOME SCI INC
                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         molecule encoding human secreted prostate for the diagnosis and treatment of disorde and autoimmune disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ς;
                                                                                                                                                                                                                                                   53.2%;
                                                                                                                                                                                                                                                 Score 800.5; DB 2
Pred. No. 4.7e-62;
                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human secreted prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an secreted prostate cancer antigen and proteins (AAB80273-AAB80321).
                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                     Indels 117;
                                                                                                                                                                                                                                                               Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer
                                                                                                                                                                                                                                     Gaps
                                                                                                                                              118
                                                                                      178
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160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brewer LA, .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Florence (
Moore PA,
Young PE;
                                                                                                   This invention describes novel isolated human secreted proteins and their encoding nucleic acid sequences. The products of the invention are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the presence or amount of expression of the new polypeptides in a sample or by determining the presence or absence of mutations in the new polynucleotides. Specific uses are absence of mutations in the new polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative.
                      disorders, developmental abnormalities and foetal deficiencies, disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-1997;
19-AUG-1997;
19-AUG-1997;
19-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUN-1998;
15-JUL-1998;
19-AUG-1997;
19-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; prevention; treatment; protein therapy; gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; developmental abnormality; foetal deficiency; blood disorder; lymphoma; leukemia; immune system disorder; autoimmune disease; hepatic disease; renal disease; inflammation; allergy; asthma; sepsis; diabetes; AIDS; Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis;
  diseases, hepatic and renal disease, lasthma, sepsis, diabetes, Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders, immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-190160/16.
N-PSDB; AAX37398.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ( HUMA - )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arthritis; psoriasis; digestive; endocrine; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 1b; Page 245-246; 280pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted protein fragment encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duan R, Er
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  human genes and the secreted polypeptides they encode diagnosis and treatment of e.g. cancers, neurological mmune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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97US-0056555.
97US-0056556.
97US-0056628.
97US-0056629.
97US-0056726.
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97US-0056369.
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98US-0092956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r R, Endress
Komatsoulis
en CA, Ruben
                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GA,
SM,
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Lafleur
Shi Y,
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 schizophrenia, osteoporosis, disorders, infections and AIL
      The concensus sequence is derived from a total of 23 HLA-A,B,C seq The protein sequences in the three extrecellular domains (alpha-1, alpha-2 and alpha-3) are shown. The example concerned the effect peptides from different HLA-A2 epitopes on cytolysis of target cel CTL of different specificities.
                                                                                                                                                                                                                                                                                                                         Key
Region
                                                                                                                                                                                                                                                                                                                                                                                             Consensus sequence alpha-3 regions of
                                                                                                  used
                                                                                                                                                                                           30-JAN-1987;
                                                                                                                                                                                                                                  11-AUG-1988
                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                      Region
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                                                                                                                               WPI; 1988-235147/33
                                                                                                                                                                      (STRD
                                                                                                                                                                                                              27-FEB-1988;
                                                                                                                                                                                                                                                     W08805784-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                          peptide corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QENQDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNSKDRKSQPMGLWRQVEGM 60
                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKDYIEFNKEIPAWVPFDPAAQITKQKWDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKDYIEFNKEIPAWVPFDPAAQITKQKWEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDWKEDSQLQKARED--METLKDIVEYYNDSNGSHVLQGRFGCETENNRSSGAFWKYYYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QENQDGRYSLTYTYTGLSKHVEDVPAFQALGSLNDLQFFRYNSKDRKSQPMGLWRQVEGM 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDWKQDSQLQKAREDIFMETLKDIVEYYNDSNGSHVLQGRFGCEIENNRSSGAFWKYYYD
                                                                                                                                                                      ) LELAND
                                                                                                                                                                                                                                                                                                                                                                          epitopes;
                                                                    9;
                                                                                                                                                   AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                 modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171
                                                                  Fig
                                                                                        or
P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                   Parham
                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , osteoporosis, arthritis, psoriasis, digestive/endocrine fections and AIDS. The human secreted proteins of the represented in AAY07744-Y07850 and the encoding nucleic resented in AAX37369-X37441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                    4.
                                                                                        auto-immune
                                                                                                                                                                       STANFORD
                                                                                                                                                                                          87US-0008846
                                                                                                                                                                                                              88WO-US00245
                                                                                                                                                                                                                                                                                                     /note="alpha-1
91..180
                                                                                                                                                                                                                                                                                   /note="alpha-2
181..272
                                                                                                                                                                                                                                                                         /note="alpha-3 region"
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          extracellular
                                                                                                                                                                                                                                                                                                                                                                                             a of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                  P,
                                                                                                 . to major histocompatibility antigen regions cytotoxic T-lymphocyte activity in e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.6%;
                                                                                                                                                                                                                                                                                                                                                                                             f peptides which constitute class I HLA molecule.
                                                                                                                                                                       JR UNIV
                                                                   English.
                                                                                                                                                  Clayberger
                                                                                         diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                                                                              region"
                                                                                                                                                                                                                                                                                                                                                                          domains
                                                                                                                                                                                                                                                                                           region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148
                                                                                                                                                                                                                                                                                                                                                                          alpha-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
.9e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                           alpha-2
                                                                                                                                                                                                                                                                                                                                                                                                       the alpha-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                   of target cells
                                                                                                                                                                                                                                                                                                                                                                           alpha-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                      alpha-2
                                                sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                               of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118
                  уd
                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΩV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                  Disclosure;
                                                                                               New recombinant DNA encoding covalently linked form of major histocompatibility complex Class I determinant, used for imm
                                                                                                                            WPI;
                                                                                                                                                                  (INRM
                                                                                                                                                                                                                             07-JUN-1995;
                                                                                                                                                                                                                                               04-JAN-2000
                                                                                                                                                                                                                                                                                                        neuroprotective.
                                                                                                                                                                                                                                                                                                                                                MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                               Kourilsky
                                                                                                                                                                            (INSP
                                                                                                                                                                                                15-NOV-1991;
05-DEC-1991;
                                                                                                                                                                                                                                                                   US6011146-A
                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                            cancer;
                                                                                                                                                                                                                                                                                                                                                                                     13-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                       AAY68268;
                                                                                                                                                                                                                                                                                                                                                                                                                          AAY68268
                                                                                                                                                                                                                                                                                                                                     immune response;
                                                                                                                                                                                                                                                                                                                    immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                                          class I; major histocompatibility complex; microglobulin; aune response; immunisation; AIDS; multiple sclerosis; toxic cer; lupus crythematosus; snake bite; cytostatic; antiviral;
                                                                                                                                                                                                                                                                                      sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRETQIVKAQSQTDREDLRTLRG----YYNQSEAGSHTIQRMYGCDVGPDGRLLRGYHQYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEGMEDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEDSQLQKA-----REDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRMEPRAPWIEQEGPEYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYSK 176
                                                                                                                            2000-125951/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETLQRADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VETRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDGKDYIALNEDLRSWTAADTAAQITQRKWEAARV-AEQLRAYLEGTCVEWLRRYLENGK
                                                                                                                                                                  __
                                                                                                                                                                                                                                                                                                                                                                   Leukocyte
                                                                                                                                                                  TRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                               ۵,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                   Column
                                                                                   e.g.
                                                                                                                                                                   NAT
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                Mottez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA,
                                                                                                                                                                                                 91US-0792473.
91US-0801818.
                                                                                                                                                                                                                             95US-0481985
                                                                                                                                                                                                                                                                                                                                                                   antigen
                                                                                                                                                                   SANTE
                                                                                      for
                                                                                                                                                                                                                                                                                                                    dermatological;
                                                                  113-116;
                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.9%;
                                                                                                                                                Ħ
                                                                                     treating cancer
                                                                                                                                                                   δ.
                                                                                                                                                                                                                                                                                                                                                                   A2/A28
                                                                                                                                                                   RECH
                                                                                                                                                Abastado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
                                                                                                                                                                                                                                                                                                                                                                                                                           365
                                                                  88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 525; DB 9; Pred. No. 9.6e-38;
                                                                                                                                                                   MEDICALE
                                                                                                                                                                                                                                                                                                                                                                  family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           AΑ
                                                                                                                                                J,
                                                                                                                                                                                                                                                                                                                   immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                   protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                    antiviral;
antiinflammatory;
                                                                                                for immune
                                                                                                                                                                                                                                                                                                                                                                    NO:100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                      antigen;
c shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                 system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176
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```

The present invention describes a recombinant DNA molecule (I) containing a sequence (Ia) that encodes an altered MHC (major histocompatibility complex) Islas I determinant (II) comprises polypeptide with alphal, alpha2, alpha3 and beta2-microglobulin domains, in which alpha3 and beta2 are covalently linked, thorous and N-termini respectively, via a nucleotide spacer sequence enc

thorough

Ģ ω

encoding

```
the antigen are associated they are recognized by a mammalian T cell CC receptor (TCR). (I) are used to produce (II) which are used to study functional interactions between the various MHC domains. They can also be used to modulate (in vivo or in vitro) the immune system by inducing CC an effector response (cytotoxicity, antibody synthesis, phagocytosis) CC of immune system cells, typically for treating, or immunising against; CC cancer, acquired immune deficiency syndrome, lupus erythematosus, CC multiple sclerosis, toxic shock and snake bite, but also for selective destruction of autoreactive cells, diagnostically to assay T cell CC receptors and to raise specific antibodies (useful for diagnosis, purification), AAZ57558 and AAY68186 to AAY68316 are sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     р,
ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        γ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                    immune response; diagnosis; antibody; immunisation; autoimmune disease acquired immune deficiency syndrome; AIDS; cytostatic; dermatological; anti-inflammatory; neuroprotective; immunosuppressive; antithyroid;
                                                                                                                                                                                                                                                                                                                                                     HLA-A2/A28 family peptide A2 (Lee) SEQ ID NO:100.
                                                                                                                                                                                                                                                                                                                                                                                        14-FEB-2000
                                                                                                                                                                          US5976551-A
                                                                                                                                                                                                                                                       vaccine; lupus erythematosus; multiple sclerosis;
                                                                                                                                                                                                                                                                                                     Major histocompatibility complex; MHC class I; MHC class II; immune response; diagnosis; antibody; immunisation; autoimmu
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY52922 standard; Peptide;
                                                             05-DEC-1991;
15-NOV-1991;
                                                                                                             07-JUN-1995;
                                                                                                                                            02-NOV-1999
                                                                                                                                                                                                             Mammalia
                                                                                                                                                                                                                                         toxic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEDSQLQKA-----REDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKYY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDGKDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQLRAYLEGTCVEWLRRYLENGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEGMEDW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLPWEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL-VETRP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVLH 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYSK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGETRKVKAHSQTHRVDLSTLRG----YYNQSEAGSHTVQRMFGCDVGSDGRFLRGYHQYA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110;
             INST PASTEUR.
INSERM INST NAT SANTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                        tumour;
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,
                                                           91US-0801818.
91US-0792473.
                                                                                                             95US-0484905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.0%;
                                                                                                                                                                                                                                         snakebite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 511; DB 21;
Pred. No. 2.4e-36;
                g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                RECH
                MEDICALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                       thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                       antigen;
                                                                                                                                                                                                                                                                                                        disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8;
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PI Kourilsky P, Mottez E, Abastado J;

XX

XX

Composition containing an antigen and altered major histocompatibility
PT Class II determinant, used to immunize against autoimmune diseases,
PT e.g. acquired immune deficiency syndrome

XX

Composition containing an antigen and altered major histocompatibility
PT Class II determinant, used to immunize against autoimmune diseases,
PT e.g. acquired immune deficiency syndrome

XX

Disclosure; Column 137-140; 96pp; English.

XX

The present invention describes a composition capable of eliciting
CC anti-major histocompatibility (MHC) antibodies. The composition
CC comprises an antigen associated with an altered MHC Class II determinant
CC (I) comprising alphal, alpha2, beta1 and beta2 polypeptide domains
CC encoded by a mammalian MHC Class II locus covalently linked to form a
CC (I) comprises an antigen estain alpha2, alpha1 and beta1 domains in
CC encoded by a mammalian MHC Class II locus covalently linked to form a
CC oplypeptide (I) containing beta2, alpha2, alpha1 and beta1 domains in
CC exequence. The resulting Antigen-MHC complex is recognizable by the T cell
CC receptor. The compositions are used for immunisation against, or
CC deficiency syndrome (AIDS), lupus erythematosus, multiple sclerosis,
CC thyroiditis, toxic shock, tumour and snakebite, depending on the nature
CC of antigen. (I) is also used to analyse functional interactions between
CC the various domains and for targeting lymphocyte receptors. Antibodies
CC against (I) are produced by usual methods of immunisation or cell fusion,
CC and may be humanised by standard methods. These antibodies are useful for
CC and may be humanised by standard methods. These antibodies are useful for
CC compositions and for targeting lymphocyte receptors. Antibodies
CC and may be humanised by standard methods of immunisation or cell fusion,
CC and may be humanised by standard methods of immunisation are useful for
CC and may be humanised by a standard methods of the present invention.

CC and column and cellular and cell
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
   260
                                                                                                                                             142
                                   235
                                                                      201
                                                                                                            177
                                                                                                                                                                                 117
                                                                                                                                                                                                                    85
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                                                                                                                                                                                                                                                                                                              GRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEGMEDW
                                                                                                                                                                                                                                                      KEDSQLQKA----REDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKYY 116
AGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLPWEPS
                                                                                                                                                                                                                  DGETRKVKAHSQTHRVDLSTLRG---YYNQSEAGSHTVQRMFGCDVGSDGRFLRGYHQYA 141
                                                                                                                                                                                                                                                                                       GSHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYW
                                                                                         NILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVLH
                                 NGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                      ETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL-VETRP
                                                                                                                                             YDGKDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQLRAYLEGTCVEWLRRYLENGK
                                                                                                                                                                               YDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYSK 176
                                                                                                                                                                                                                                                                                                                                                              110;
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                               34.0%;
                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                                                                                                                                                                                                                                                                               Score 511; DB 21, Pred. No. 2.4e-36,
                                                                                                                                                                                                                                                                                                                                                            Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                Length 365;
                                                                                                                                                                                                                                                                                                                                                              Indels
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RESULT 8
AAB58683
ID AAB58683 standard; protein; 365 AA.

XX
AC AAB58683;
XX
AC AAB58683;
XX
BT 13-MAR-2001 (first entry)
XX
DE HLA-A2/A28 protein #4.
XX
DE MAJor histocompatibility complex; MHC class I; immune; snake bite;
XX
KW T cell mediated autoimmune disease; AIDS; lupus erythematosus;
XX
OS Unidentified.
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RESULT 9
ABB39399
ID ABB3
XX
AC ABB3
XX
DT 04-F
XX
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Best Local
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07-SEP-1993;
05-DEC-1991;
07-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a major histocompatibility complex (MHC) class I determinant, which has alpha_1 alpha_2 alpha_3 and beta2-microglobulin polypeptide domains encoded by a mammalian MHC class I locus. The MHC class I determinants are useful for activating the immune system and presenting antigens to the immune system to elicit an antigenic response. The MHC class I determinants are also useful for treating diseases, e.g. T cell mediated autoimmune disease, AIDS, lupus erythematosus, toxic shock or snake bite. The altered MHC class I determinants and compositions containing antigens bound to the determinants are useful in diagnostic applications, e.g. altered determinants may be used to target lymphocyte receptors and the resulting bound determinant can be assayed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New altered major histocompatibility complex (MHC) class I determinant useful for eliciting an immune response and/or for immunizing against or treating diseases, for example, multiple sclerosis, AIDS, toxic shock or snake bite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
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            04-FEB-2002
                                                      ABB39399 standard;
                                  <u>аввз9399;</u>
                                                                                                            260
                                                                                                                                  235
                                                                                                                                                       201
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                                                                                                                                                                                                  142
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                                                                                                                                                                                                                                                              KEDSQLQKA-----REDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKYY 116
                                                                                                                                                                                                                                                                                      GSHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYW
                                                                                                                                                                                                                                                                                                        GRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEGMEDW 63
                                                                                                                                                                            NILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVLH
                                                                                                                                                                                                             YDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYSK 176
                                                                                                                                                                                                                                            DGETRKVKAHSQTHRVDLSTLRG---YYNQSEAGSHTVQRMFGCDVGSDGRFLRGYHQYA 141
                                                                                                            AGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLPWEPS
                                                                                                                                 NGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                       ETLORTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL-VETRP
                                                                                                                                                                                                  YDGKDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQLRAYLEGTCVEWLRRYLENGK
                                                                                                                                                                                                                                                                                                                              al Similarity
110; Conserv
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NAT SANTE & RECH MEDICAL.
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            (first entry)
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91US-0801818.
93US-0072787.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-33; 105pp; English
                                                      Peptide;
                                                                                                                                                                                                                                                                                                                                         34.0%;
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                                                                                                                                                                                                                                                                                                                                45;
                                                       93
                                                                                                                                                                                                                                                                                                                                         Score 511;
Pred. No. 2.
                                                       A
                                                                                                                                                                                                                                                                                                                                 Mismatches
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   ABB24181
XX
AC ABB
XX
AC ABB
XX
DT 23-
DT 23-
XX
EN Prc
XX
Hun
KW Ca1
KW Ca1
KW Co1
XX
COS Hor
XX
NO:
WO:
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WO200157274-A2

Human; gene expression; heart; microacardiovascular disease; hypertension;

heart; microarray; vascular systenypertension; cardiac arrhythmia

vascular system;

Protein #6180 encoded by probe for measuring heart cell gene expression.

23-JAN-2002

(first

entry)

congenital heart

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RESULT
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                                                                                                                                                                                                                                                Matches
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                              measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver - \,
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                                                                                                                                                                                                                                                                                                                  Sequence
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ABB24181;
                                 ABB24181 standard;
                                                                                                                                                244
                                                                                                                                                                                                  184 PPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGQVQEPELRGDVLHNGNGTYQSW 243
                                                                  10
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                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates
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                                                                                                                                    VVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-483447/52
                                                                                                                 VVVAVPPODTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                 foetal liver;
                                                                                                                                                                                                                                                l Similarity
92; Conserv
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO 32034; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DK,
                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene expression;
                                                                                                                                                                                                                                                                 33.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human foetal liver single exon
                                                                                                                                                                                                                                                     <u>ب</u>
                                  93
                                                                                                                                                                                                                                                 Score 510; DB 22;
Pred. No. 4.7e-37;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
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                                                                                                                                                     276
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RESULT 11
AAM60079
ID AAM60
XX AAM60
XX O5-NC
XX O5-NC
XX Human
XX Human
XX micro
KW Human
XX epile
XX Homo
XX
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Best Local
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA4135). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at from int/mih/mih/shad not segmence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                      Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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30-JAN-2001; 2001WO-US00667.
                                           09-AUG-2001
                                                                                  WO200157275-A2
                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                            05-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 PPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGQVQEPELRGDVLHNGNGTYQSW 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS 276
                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGEVQEPELRGDVLHNGNGTYQSW 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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98.9%;
                                                                                                                                                                                                                                                   single exon
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                                                                                                                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 510; DB 22;
Pred. No. 4.7e-37;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for analyzing gene expression in
                                                                                                                                                                                                                                                 probe encoded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                                                                   ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
  밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DЬ
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RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system which may enable the diagnosis and improved treatment of nervous system.
                                                                                                                                                                                                                microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epilepsy and cancers. The present sequence is a the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single exon nucleic acid
                      04-OCT-
                                                                                                                   30-JAN-2001;
                                                                                                                                           09-AUG-2001
                                                                                                                                                                 WO200157276-A2
                                                                                                                                                                                          Homo
                                                                                                                                                                                                                           Human; bone
                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                            06-NOV-2001
                                                                                                                                                                                                                                                                                                                          AAM72688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-483446/52.
(MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                  184 PPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGQVQEPELRGDVLHNGNGTYQSW 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                             244 VVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                     VVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SG,
                                                                                                                                                                                                                                                   bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92; Conserv
MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ
                                                                                                                                                                                                                                                   marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                           marrow expressed exon;
                                                                                                                                                                                                                 cancer;
                     2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632368.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                   2001WO-US00668
                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DK,
                                                                                                                                                                                                                                                   expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO:
                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                leukaemia; lymphoma; myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥,
                                                                                                                                                                                                                                                                                                                          93
                                                                                                                                                                                                                                                   probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 510; DB 22;
Pred. No. 4.7e-37;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    650pp + Sequence
                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                   encoded
                                                                                                                                                                                                                           gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR;
                                                                                                                                                                                                                                                                                                                                                                                     93
                                                                                                                                                                                                                                                                                                                                                                                                             276
                                                                                                                                                                                                                                                 protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                                                   NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        samples
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RESULT 13
AAM32919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
  The
                                                                                                                                   04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single eanalyzing gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn
                   Claim
                                     analyzing
                                                                                                                                                                                                                                                                               genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example
                                                                                                                           04-OCT-2000;
                                                                                                                                                                                                      30-JAN-2001;
                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                           WO200157272-A2
                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                           Peptide #6956
                                                                                                                                                                                                                                                                                                                              17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                   AAM32919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 PPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGQVQEPELRGDVLHNGNGTYQSW 243
                                                                                                                                                                                                                                                                                                                                                                                                                                  244
                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention provides a number of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                         VVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SG,
                                                                                                                                                                                                                                                                                                                                                                                                                 VVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                   2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGEVQEPELRGDVLHNGNGTYQSW 60
                                   genome-derived single exon
ling gene expression in huma
                                                                                                                                                                                                                                                                               microarray;
c disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
92; Conser
                                                                                                        MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel
                   SEQ
                                                                                     Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:
                                                                                                                                  2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                      2001WO-US00663
                                                                                                                                                                                  2000US-0180312
                    H
                                                                                                                                                                                                                                                                                                           encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DK,
                   No
                                                                                     DK,
                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.9%;
98.9%;
                                                                                                                                                                                                                                                                                                           by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32994; 658pp + Sequence Listing;
  relates
                                                                                      Chen
                                                                                                                                                                                                                                                                                        placenta;
                                                                                     ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Σ
                  654pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon nucleic acid probes useful n human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                    93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 4.7el; Mismatches
                                      human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
  ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank
                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                      Rank
single exon
                                                nucleic acid
                   English.
                                                                                                                                                                                                                                                                                                          measuring placental gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    510; DB 22;
No. 4.7e-37;
                                      placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR;
                                                                                                                                                                                                                                                                                          antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                 93
                                                                                                                                                                                                                                                                                                                                                                                                                                   276
  nucleic
                                                probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment of cancers
  acid
                                                useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93
 probes
                                                                                                                                                                                                                                                                                                             expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
 (SENP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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RESULT 14
ABG42512
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32333x3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicoytosis; Jupphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                         Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             see AAI31315-AAI57546). The present sequence is a peptide encoded by such probe. The probes are useful for producing a microarray for preducting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
                                                                              Claim
                                                                                                                    Spatially-addressable set of single exon nucleic acid
                                                                                                                                                                                                                                                                     30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                             WO200186003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG42512 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human genetic disorders.
                                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                                           21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                       30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                  15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG42512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 PPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGQVQEPELRGDVLHNGNGTYQSW 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                     invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGEVQEPELRGDVLHNGNGTYQSW
                                                                               27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
92; Conser
                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane
                                                                                                                                                                                                    MOLECULAR DYNAMICS INC
                                                                               SEQ
                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 AA;
                                                                                                                                                                                                                             ; 2000US-180312P.
; 2000US-207456P.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-234687P.
; 2000US-236359P.
; 2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                         expression in human
                                                                                                                                                                                                                                                                                                                                         2001WO-US00665
                                                     relates to
                                                                               IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease
                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide;
                                                                               32177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                γd
                                                                                                                                                                          Chen
                                       a spatially-addressable set of single measuring gene expression in a sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome-derived single exon probe SEQ ID 32177.
                                                                                                                                                                            Σ,
                                                                              634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 510; DB 22;
Pred. No. 4.7e-37;
                                                                                                                                                                            Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                       Lung
                                                                                                          samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                       probes, used
                                                     single
                                          derived
                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 derived
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of

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RESULT 15
AAUJ32882
ID Z8882
XX AUJ32
AC AAUJ32
AC AAUJ32
XX 18-DE
DT 18-DE
XX Human
KW Human
KW Stem
KW Stem
KW Stem
OS Homo
XX WÖ200
XX WÖ200
XX YS 16-AF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed encoded that the protein have the sequence data for this patent did not form part.
                                                                                                                                                                                                                                                                                                                            Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemi
                                      16-APR-2001; 2001WO-US08656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel human secreted polypeptides. The CC polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated CC with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cclls expressing the proteins are useful for identifying a therapeutic agent CC for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising CC the nucleic acids encoding the polypeptides and cells genetically cengineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and CC therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in CC bone, cartilage, tendon and/or stimulation; as anti-inflammatory agents; and CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid CC sequences of novel human secreted proteins of the invention.
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                 Matches 110;
                                                   Query Match
                                                                                                                                                                     TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PARTICL NUMBER: US 07/792,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Fioppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
                                                                                                                                                                                                                                    TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsy, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 NILDRODPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVLH
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                                  Local Similarity
                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 03495.0106-03000
                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 15-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08, FILING DATE: 07-JUNE-1995
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                                                                                                                                                                                                                                                                                                              NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                             TOPOLOGY:
                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Finnegan, Henderson, Farabow, ADDRESSEE: Dunner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETLQRADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VETRP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDGKDYIALNEDLRSWTAADTAAQITQRKWEAARV-AEQLRAYLEGTCVEWLRRYLENGK 176
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                                                                                                                                        amino acid
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5976551
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                 Conservative
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                                                                                                        peptide
                                  34.0%;
39.0%;
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                                                                                                                                                                                                 100:
                 45;
                              Score 511; DB 2;
Pred. No. 3.2e-40;
                 Mismatches 111;
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                                               Length 365;
               Indels
     16;
Gaps
             8;
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Query Match
Best Local Similarity
                                                                                                                  TELEFAX: 202-400 ID NO: 1
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 365 amino acids
                                                                                                                                                                                                                                  NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 034
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
OPERATOR NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 0
FILING DATE: 05-DEC-1991
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Phillipe
APPLICANT: Kourilsky, Phillipe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 YDGKDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQLRAYLEGTCVEWLRRYLENGK 200
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US (FILING DATE: 15-NOV-1991 CLASSIFICATION: 435
                                                                                                TOPOLOGY:
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5. 6011146
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                                                                                                                                                                                                                    202-408-4000
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                                                                           peptide
  34.0%;
39.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 07/801,818
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                    Score
                    511;
l; DB 3;
. 3.2e-40;
                  Length 365;
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US-08-370-476-100
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             TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ojcius, Da APPLICANT: Casrouge,
SEQUENCE CHARACTERISTICS:
                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       FILING DATE: 05-DEC-PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polocial
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                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
                                                                                                      NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                   TELEPHONE:
                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYW 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEGMEDW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLPWEPS 301
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Ojcius, David
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                                                       202-408-4000
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US-08-484-905-98
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                       NAME:
                                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 05-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 KEDSQLQKA-----REDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKYY 116
                                 REFERENCE/DOCKET NUMBER: 03.
                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/484,905 FILING DATE: 07-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                              CLASSIFICATION:
                                                                                                                                FILING DATE:
                                                                                                                                                    APPLICATION NUMBER: US 07/792,473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVLH 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYSK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGETRKVKAHSQTHRVDLSTLRG---YYNQSEAGSHTVQRMFGCDVGSDGRFLRGYHQYA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEGMEDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDGKDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQLRAYLEGTCVEWLRRYLENGK
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20005-3315
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                                                                                                                              15-NOV-1991
                                                                       Jane E.
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                                     03495.0106-03000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
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                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
                                                                                                                                                             CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                              CLASSIFICATION:
                                                                                                                            APPLICATION NUMBER: US 07/801,818 FILING DATE: 05-DEC-1991
                                                                                                                                                                                                APPLICATION NUMBER: US/08, FILING DATE: 07-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                STATE:
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               NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYSK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGETRKVKAHSQTHRVDLSTLRG---YYNQSEAGSHTVQRMYGCDVGSDWRFLRGYHQYA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYW 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETLORTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWORDGEDOTODTEL-VETRP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDGKDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQLRAYLEGTCVEWLRRYLENGK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLPWEPS 301
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                                                                                                                                                                                                                                                                                                                                  20005-3315
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Potter, Jane E. R. RATION NUMBER: 33,332
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Best Local Similarity
Matches 112; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 98,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mottez, ESCELLE
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Phillipe
APPLICANT: MOUTILSKY, Phillipe
APPLICANT: MOUTILSKY, Phillipe
APPLICANT: MOUTILSKY, Phillipe
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                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                    FILING DATE: 05-DEC-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (1
                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 QDAYDGKDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQWRAYLEGTCVEWLRRYLE 197
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ADDRESSEE:
STREET: 130
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                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
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                      CLASSIFICATION:
                                        FILING DATE:
                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 05-DEC-1991
                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                     SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KED-----SQLQKAREDMETLKDIVEYYNDSN-GSHVLQGRFGCEIENNRSSGAFWKYY- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSKNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGD 231
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1300 I Street, N.W., Suite 700
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                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                             Finnegan, Henderson, Farabow,
    INFORMATION
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                                        15-NOV-1991
                                                                                                                                                                                           07-JUN-1995
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                                                                                                                                     US 07/801,818
                                                                                                                                                                                                                 US/08/481,985B
                                                          US 07/792,473
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Phillipe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 1: MOLECULE TYPE:
                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER . 117.018.481 0458
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CITY: Washington
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                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Finnegan, Henderson, Farabow, ADDRESSEE: Dunner
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FILING DATE:
                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL-VETRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGETRKVKAHSQTHRVDLSTLRG---YYNQSEAGSHTVQRMYGCDVGSDWRFLRGYHQYA 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLPWEPS 301
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20005-3315
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15-NOV-1991
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               US 07/792,473
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Best Local S
Matches 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 98, Application US/08370476 Patent No. 6153408
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                                                                                                                                                                                                                                                                                                                                        APPLICANT: KOUTILSK,
APPLICANT: KOUTILSK,
APPLICANT: LONE, YU
APPLICANT: Ojcius, I
APPLICANT: Casrouge,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide
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                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                STATE: D.C.
ZIP: 20005-3315
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nes 112; Conserv
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REFERENCE/DOCKET NUMBER: 03
                                CLASSIFICATION:
                                                     FILING DATE:
                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                     STREET:
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APPLICATION NUMBER:
                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRPAGDGTFQKWVAVVVPSGQEQRYTCHVQHEGLPKPLTLPWEPS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL-VE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEGMEDW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSKNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGD 231
                                                                                                                                                                                                                                  Washington
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amino acid
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1300 I Street,
                                                                                                                                                                                                                                                                                                                                                                              Casrouge,
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Kourilsky, Phillipe
Lone, Yu-Chun
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                                                                                                      PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                     Finnegan, Henderson, Farabow,
                                    435
                                                                                                                                                                                                                                                                                                                                                               Altered Major Histocompatibility Complex
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                                                                                                                                                                                                                                                                                                                               127
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US 08/117,575
                                                                    US/08/370,476
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RESULT 10
US-08-370-476-102
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                                                                                                                                                                                                                                                                                                                                                        Sequence 102, Application US/08370476 Patent No. 6153408
                                                                                                                                                                                                                                                                                                                                    Patent No. 6153408
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202,408-4000
                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-NOV-1991 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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   COMPUTER:
                                                    STATE: D.C.
ZIP: 20005-3315
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                                                                                         CITY
                                                                                                       STREET:
                                                                                                                                            ADDRESSEE:
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                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL-VETRP 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLPWEPS 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDGKDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQLRAYLEGTCVEWLRRYLENGK 200
                                                                                   Washington
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                                                                                                      E: Dunner
1300 I Street,
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Kourilsky, Phillipe
Lone, Yu-Chun
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   IBM PC
                                                                                                                                        Finnegan, Henderson, Farabow,
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38.7%;
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Pred. No. 7.7e-40;
7; Mismatches 110
                                                                                                       Suite 700
                                                                                                                                          Garrett
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US-08-484-905-101
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                                                                                                                                                                                                                   Sequence 101, Application US/08484905 Patent No. 5976551
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Matches 112;
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Best Local :
                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Mottez
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                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                            APPLICANT:
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APPLICATION NUMBER: US 0
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
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PRIOR APPLICATION DATA:
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 STREET:
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                  ADDRESSEE: Finnegan, Henderson, Farabow, ADDRESSEE: Dunner
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1300 I Street,
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                                                                                                      Abastado, Jean-Pierre
Kourilsky, Philippe
VERWION: An Altered Major Histocompatibility
VERWION: Complex(MHC) Determinant and Method:
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UMBER: US 08/072,787
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N.W., Suite
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                                                                                                                                                                                                           US-08-481-985B-101
                                                                                                                                                   Sequence 101, Application US/08481985B Patent No. 6011146 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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NAME: Potter, Jane E. R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy Disk
                                                      TITLE OF INVENTION:
                                                                                        APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Phillipe
                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                        195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 ----YYYDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRK 170
                                                                                                                                                                                                                                                                                            255
                                                                                                                                                                                                                                                                                                                                                                                                       171 YLKYSKNILDRODPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                               136 GYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKWETAHV-AEQLRAYLEGTCVEWLRR
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ZIP: 20005-3315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                            RGDVLHNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGETRKVKAHSQTHRVDLSTLRG---YYNQSEAGSHLVQRMYGCDV-----GFDWRFLR 135
                                                                                                                                                                                                                                                                                        -VETRPAGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLPWEPS
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Finnegan, Henderson, Farabow, Garrett &
                                                                            Altered Major Histocompatibility Complex
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                                        148
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US-08-370-476-101
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                                                                   Sequence 101, Application US/08370476 Patent No. 6153408 GENERAL INFORMATION:
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Best Local S
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                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
OTHER PRIOR OF TARMY NUMBER: US 07/792,473
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
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hes 110;
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9TD: 20005-3315
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REGISTRATION NUMBER: 25,146
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                                                                                                                                                                                                                                                                                                                                                                                                       DGETRKVKAHSQTHRVDLSTLRG---YYNQSEAGSHLVQRMYGCDV-----GFDWRFLR 135
                                                                                                                                                                                            -VETRPAGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLPWEPS
                                                                                                                                                                                                                           RGDVLHNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
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                                                                                                                                                                                                                                                                                                                                GYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKWETAHV-AEQLRAYLEGTCVEWLRR 194
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1300 I Street, N.W.,
Mottez, Estelle
Abastado, Jean-Pierre
Kourilsky, Phillipe
Lone, Yu-Chun
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07-JUN-1995
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38.2%; Pred. No. 1.2e-39;
tive 44; Mismatches 106
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APPLICANT: APPLICANT: APPLICANT:

Ojcius, David Casrouge, Armanda

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                  US-08-484-905-104
                                 RESULT 14
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Best Local Similarity
Matches 110; Conserv
Sequence 104, Application US/08484905
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INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
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APPLICATION NUMBER: US 0:
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
05 07/801,818
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REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05
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                                                                                                                                                                                                                                                                                                 DGETRKVKAHSQTHRVDLSTLRG---YYNQSEAGSHLVQRMYGCDV-----GFDWRFLR 135
                                                                                                                                                                                                                                                                                                                                                                                                      GRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEGMEDW 63
                                                                                                                                                                                           YLKYSKNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPEL 228
                                                                                                                   RGDVLHNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS 276
                                                                                                                                                        YLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTEL
                                                                                      -VETRPAGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLPWEPS
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Pred. No. 1.2e-39;
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GENERAL INFORMATION:
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Best Local Similarity 39.3%;
Matches 112; Conservative 4
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SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
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APPLICANT: Abastado, Jean-I
APPLICANT: Kourilsky, Phil
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CURRENT APPLICATION DATA
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ZIP: 2
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CLASSIFICATION:
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                         VLHNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS 276
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Kourilsky, Philippe
VENTION: An Altered Major Histocompatibility
AN EXPRISON: Complex(MHC) Determinant and Methods for Using the
VENTION: Determinant
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pred. No. 1.5e-39;
42; Mismatches 109
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US-08-481-985B-104
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION UNMBER: US 07/
APPLICATION NUMBER: US 07/
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25.146
REFERRNCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
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CORRESPONDENCE ADDRESS:
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257 TRPAGDGTFQKWVAVVVPSGQEQRYTCHVQHEGLPKPLTLPWEPS 301
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Abastado, Jean-Pierre
Kourilsky, Phillipe
VENTION: Altered Major Histocompatibility Complex
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RESULT 2 US-09-864-761-39479 ; Sequence 39479, Application US/09864761

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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
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CURRENT FILING DATE: 2001-05-23
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-29
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 11

OTHER INFORMATION: EXPRESSED IN ETHAL LIVER, SIGNAL = 5.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.88

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.94

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.79

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7

OTHER INFORMATION: SWISSPROT HIT: P25311, EVALUE 5.00e-53
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                              184 PPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGQVQEPELRGDVLHNGNGTYQSW 243
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APPLICATION NUMBER: US 09/608,408
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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L INFORMATION:
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PPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGEVQEPELRGDVLHNGNGTYQSW 60
                                                                                                    92;
                                                                                                                         Similarity
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Pred. No. 4
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                                                                                                                                                                                                                                                          Sequence 5, Application US/10073300
publication No. US20030003535A1
GENERAL INFORMATION:
APPLICANT: Reiter, Yoram
TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
FILE REFERENCE: 02/23339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10073300 Publication No. US20030003535A1 GENERAL INFORMATION:
                                                                                                                                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 5
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Matches
                Query Match
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CURRENT FILING DATE: 2002-06-25
NUMBER OF SEQ ID NOS: 20
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                      LENGTH: 415
TYPE: PRT
                                                                                     OTHER INFORMATION: human beta2 microglobulin linked to MHC
                                                                                                       FEATURE:
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;al Similarity 37.9%; Pred. No. 5.7e-34;
107; Conservative 48; Mismatches 111;
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al Similarity
107; Conser
 Conservative
                  32.7%;
   48;
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Pred. No. 9
   Mismatches
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                  DB 9;
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                                        NUMBER
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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                                                                                            FILING DATE: 2000-06-30
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APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00670
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FILING DATE: 2000-08-03
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                                        SEQ ID NOS: 49117
                   Annomax Sequence Listing
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Hanzel, David K.
Chen, Wensheng
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Patent No. US20020051989A1
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Best Local
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PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PAFARATT
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CURRENT FILING DATE: 2001-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHOD FOR BREEDING AND GENOTYPING CHICKENS AND PROBES THEREFO FILE REFERENCE: 1954-310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Miller, Marcia APPLICANT: Goto, Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 332
TYPE: PRT
ORGANISM: Gallus
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                                                                                                                                                          122 YIEFNKEIPAWYPFDPAAQITKQKWEAEPYYYQRAKAYLEEECPATLRKYLKYSKNILDR 181
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QSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWE: | |:| | | |:|:|| | | : ||
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                                                       RVQPEVRVWGKEADG-ILTLSCHAHGFYPRPITISWMKDGMVRDQETRWGGIVPNSDGTY
                                                                                                                             FLAFDMDTMTFTAADPVAEITKRRWETEGTYAERWKHELGTVCVQNLRRYLEHGKAALKR
                                                                                                                                                                                                                                                                           GSHSLRYFLTGMTDPGPGMPRFVIVGYVDDKIFGTYNSKSRTAQPIVEMLPQEDQEHW--
                                                                                                                                                                                                  DTQTQKAQGGERDFDWNLNRLPERYNKSKGSHTMQMMFGCDILEDGSIRGYDQYAFDGRD 118
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                                                                                        QDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGQVQEPELR-GDVLHNGNGTY
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N: EXPRESSED IN PLACENTA, SIGNAL = 6.5

N: EXPRESSED IN LUNG, SIGNAL = 7.2

N: EXPRESSED IN HELA, SIGNAL = 7.2

N: EXPRESSED IN ADULT LIVER, SIGNAL = 7.6

N: EXPRESSED IN HEART, SIGNAL = 7.6

N: EXPRESSED IN BRAIN, SIGNAL = 8.

N: EXPRESSED IN BRAIN, SIGNAL = 8.00e-4.
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Pred. No. 2.6e-32;
4; Mismatches 4
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Pred. No. 4e-31;
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8.00e-47
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                                                    ; ORGANISM: Homo sapiens US-09-925-301-1431
                                                                                                                                                                                                                                                                                                                                          Sequence 1431, Application Patent No. US20020052308A1 GENERAL INFORMATION:
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LENGTH: 334
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                                                                                                       SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1431
LENGTH: 271
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                  Query Match
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CURRENT FILING DATE: 2001-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHOD FOR BREEDING AND GENOTYPING CHICKENS AND PROBES THEREFOR FILE REFERENCE: 1954-310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Miller, Marcia APPLICANT: Goto, Ronald
Best Local Similarity
                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins
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                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US00/05882 PRIOR FILING DATE: 2000-03-08 PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
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                                                                                                                                                                                                                                                                                       FILE REFERENCE: PA106
                                                                                                                                                               NUMBER OF SEQ ID NOS: 1694
                                                                                          TYPE: PRT
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Pred.
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 372;
No. 5.
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                  Length 271;
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US-09-847-172-21;
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PRIOR APPLICATION NUMBER: 09/153,586
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/064,552
PRIOR APPLICATION NUMBER: 60/064,555
PRIOR APPLICATION NUMBER: 60/064,555
PRIOR FILING DATE: 1997-10-10
NUMBER OF SEO ID NOS: 30
                                                         RESULT 10
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SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation of TITLE OF INVENTION: antigen-specific T-Cells FILE REFERENCE: 48823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/858,580 CURRENT FILING DATE: 2001-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 18
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 DRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVLHNGN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 147
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                                                                                                                                                                                                                                                               DRNTQIFKTNTQTYRENLRIALRYYNQSEAGSHIIQRMYGCDLGPDGRLLRGHDQSAYDG 120
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                                                                                                                                                                                    KDYIALNEDLSSWTAADTAAQITQRKWEAARV-AEQLRAYLEGLCVEWLRRYLENGKETL 179
                                                                                                                                                                                                                         KDYIEFNKEIPAWVPFDPAAQITKOKWEAEPVYVQRAKAYLEEECPATLRKYLKYSKNIL 179
                                                                                                                                                                                                                                                                                                KEDSQLQKARED--METLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKYYYDG 119
                                                                                                                                                                                                                                                                                                                                                                         GRYSLTYTYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEGMEDW 63
                                                                                                                                                   DRQDP 184
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Pred. No. 8.8e-20;
"'-matches 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09810560 Patent No. US20020052487A1
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                                                                                                                                           SEQ ID NO 8
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APPLICANT: BURROWS, GREGORY G.
APPLICANT: VANDENBARK, ARTHUR A.
TITLE OF INVENTION: RECOMBINANT MHC MOLECULES USEFUL FOR MANIPULATION OF
TITLE OF INVENTION: CELLS
FILE REFERENCE: 899-58137
CURRENT APPLICATION NUMBER: US/09/847,172
CURRENT APPLICATION NUMBER: US/09/847,172
                       Query Match
  Best Local Similarity
                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 08/406,057
PRIOR FILING DATE: 1995-03-17
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                           APPLICANT: KIRSZENBAUM, MAREK
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G GENE AND THEIR APPLICATIONS
FILE REFERENCE: 204824U50 DIV
CURRENT APPLICATION NUMBER: US/09/810,560
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: US 08/958,316
PRIOR FILING DATE: 1997-10-27
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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APPLICANT: MOREAU, PHILIPPE
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PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: US 60/064,555
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/064,552
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                                                                                                                                                                   SOFTWARE:
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TYPE: PRT
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                                                                            LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 8.8e-20;
""" rmatches 72;
Score 235.5; DB 1
Pred. No. 6.8e-13;
                   DB 10;
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US-09-864-761-39405
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SOFTWARE: Annous
SEQ ID NO 39405
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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PRIOR APPLICATION NUMBER: US
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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                 ORGANISM: Homo sapiens FEATURE:
OTHER INFORMATION: MAP TO AC006329.2
                                                     TYPE: PRT
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                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
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                                                                                                                                                               APPLICATION NUMBER: US 09/774,203
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                                                                                                          Sequence Listing Engine vers.
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 120
LENGTH: 92
TYPE: PRT
ORGANISM: Homo sapiens
US-10-016-634A-120
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US-10-016-634A-120
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US-09-796-692-799
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Best Local Similarity
                                                                                                                                                                                                                                       Sequence 799, Appublication No.
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CURRENT APPLICATION NUMBER: US/10/016,634A
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: US 60/244,258
PRIOR FILING DATE: 2000-10-31
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/190,479
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EXPRESSED IN LUNG, SIGNAL = 6.1

EXPRESSED IN HEART, SIGNAL = 73

EXPRESSED IN FETAL LIVER, SIGNAL = 2

SWISSPROT HIT: Q64726, EVALUE 6.00e-27

EST_HUMAN HIT: BF677910.1, EVALUE 2.00e-39
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57.1%;
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PRIOR APPLICATION NUMBER: 60/223,378

PRIOR FILING DATE: 2000-08-07

NUMBER OF SEQ ID NOS: 9597

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 799

LENGTH: 110
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR TILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
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Best Local Similarity 41.0%;
Matches 43; Conservative 1
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
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                                           PRIOR ETLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/202,084
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OR FILING DATE: 2000-04-28
OR APPLICATION NUMBER: 60/200,779
OR FILING DATE: 2000-04-28
OR APPLICATION NUMBER: 60/200,999
OR FILING DATE: 2000-05-01
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FILING DATE: 2000-04
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FILING DATE: 2000-05-04
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FILING DATE: 2000-05-22
                                                                                                                  APPLICATION NUMBER: 60/200,999
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                                                                                                                                        FILING DATE: 2000-04-28
                 APPLICATION NUMBER: FILING DATE: 2000-0
                                                                                                                                                           APPLICATION NUMBER: 60/200,779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Algate, Paul A.
NUMBER: 60/218,950
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                                         60/206,201
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; Pred. No. 1.6e-10;
17; Mismatches 42;
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Title:
Perfect score:
Sequence:
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Maximum Match 100
Listing first 45:
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Maximum DB seq length: 2000000000
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2: pir2:*
3: pir3:*
4: pir4:*
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1504
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Gapop 10.0 , Gapext 0.5
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Match Length
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GenCore version 5.1.3 Coppright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

34422 residues	ALIGNMENTS
chosen parameters: 283224	
5	RESULT 1 A54175 Zino-alpha-2-qlycoprotein precursor - human
0.00	N;Alternate names: class I histocompatibility complex alpha chain homolog C;Species: Homo sapiens (man)
00% 5 summaries	C;Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999 C;Accession: A54175; A49357; I52248; S17564; A31080; PC2210; I65208; JQ0946 R;Ueyama, H.; Deng, H.X.; Ohkubo, I.
	A;Title: Molecular cloning and chromosomal assignment of the gene for human Zn-alpha A;Reference number: A54175; MUID:94059971; PMID:8241150 A;Accession: A54175 A;MOID:94059971; PMID:8241150 A;Accession: A54175 A;MOID:94059971; PMID:8241150 A;Accession: A54175 A;MOID:9405971; PMID:8241150 A;Accession: A54175
results predicted by chance to have a	A;Cross references: GB:D14034: NTD:a456585
of the total score distribution.	A; Note: Sequence extracted from NCBI backbone (NCBIN:140118, NCBIP:140119) A; NCF: Sequence extracted from NCBI backbone (NCBIN:140118, NCBIP:140119) R; Preije, J.P.; Fueyo, A.; Uria, J.A.; Velasco, G.; Sanchez, L.M.; Lopez-Boado, Y.S.;
SUMMARIES	A; Title: Human Zn-alpha-2-glycoprotein: complete genomic sequence, identification of A; Reference number: A49357; MUID:94140356; PMID:8307568 A; Accession: A49357
ID Description	A; Residues: 1-298 <fre></fre>
	A;Cross-references: GB:X69953; NID:g467670; PIDN:CAA49574.1; PID:g467671
JX0352 zinc-alpha 2-glyco	R;Deyalla, H.; NIWA, M.; TAGA, T.; SASAKI, M.; UIRKUD, I. Biochem. Biochys. Res. Commun. 177. 696-703. 1991
	A; Title: Cloning and nucleotide sequence of a human 2n-alpha2-glycoprotein cDNA and c
137515 Lymphocyte antigen HC class I histoc	A;Recerence number: 152248; MUID:91264833; PMID:2049092 A;Accession: 152248
мнс	A;Status: translated from GB/EMBL/DDBJ
I80169 Class I histocompa	A; Molecule Type: mkNA A. Residues: 4-298 CUEY2>
	A;Cross-references: GB:D90427; NID:g220150; PIDN:BAA14417.1; PID:g220151; GB:M76707;
I80165 Class I histocompa	A;Note: submitted to JIPID, June 1991 R:Freije, J.P.: Fuevo, A.: Uria, J.: Lopez-Otin, C.
мнс	FEBS Lett. 290, 247-249, 1991
I54493 MHC class I histoc I56116 MHC HLA-B27-HS - h	A;Title: Human Zn-alpha(2)-glycoprotein cDNA cloning and expression analysis in benig A;Reference number: S17564; MUID:92008677; PMID:1915885
MHC	A; Accession: \$17564
I54416 HLA-AW24 protein -	A; Molecule type: mRNA
I80167 class I histocompa	A; Residues: 'MWAS', 1, 'S', 3-4, 'L', 6-208 CFR2>
HLHUB2 MHC class I histoc	R;Araki, T.; Gejyo, F.; Takagaki, K.; Haupt, H.; Schwick, H.G.; Buergi, W.; Marti, T.
I54418 MHC class I histoc I72755 HLA-B*5602 - human	Proc. Natl. Acad. Sci. U.S.A. 85, 679–683, 1988 A;Title: Complete amino acid sequence of human plasma Zn-alpha-2-glycoprotein and its
	A;Reference number: A31080; MUID:88124905; PMID:3422450
S06424 MHC class T histoc	A;Accession: Asiubu
MHC class I	A; Residues: 21-84, 7E', 86-95, 98-243, 'Q', 245-298 <ara></ara>
172753 HLA-B*5502 - human 156130 HLA-B*5401 - human	R;Takagaki, M.; Honke, K.; Tsukamoto, T.; Higashiyama, S.; Taniguchi, N.; Makita, A.; Biochem. Biophys. Res. Commun. 201, 1339–1347, 1994

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A;Title: Zn-alpha2-glycoprotein is a novel adhesive protein.
A;Reference number: pC2210; MUID:94296408; pMID:802,4578
A;Recession: pC2210
A;Molecule type: protein
A;Residues: 239-256,'D',258-265 <TAK>
A;Residues: 239-258,'D',268-265 <TAK>
A;Residues: 239-258,'D',268-265 <TAK>
A;Residues: 239-258,'D',258-265 <TAK>
A;Residues: 239-258,'D',258-265,'D',258-265,'D',258-265,'D',258-265,'D',258-265,'D',258-265,'D',258-265,'D',258-265,'D',258-265,'D',258-265,'D',258-265,'D',258-265,'D',258-265,'D',258-265,'D',258-265,'D',258-265
                                                                                                                                                                                                R;Ueyana, H.; Naitoh, H.; Ohkubo, I.
J. Biochem. 116, 677-681, 1994
A;Title: Structure and expression of rat and mouse mRNAs for Zn.
A;Reference number: JX0352; MUID:9515283; PMID:7852290
A;Reference number: JX0353
A;Molecule type: mRNA
A;Residues: 1-279 <UEYA
A;Cross-references: DDBJ:D21058
A;Cross-references: DDBJ:D21058
A;Experimental source: liver
C;Superfamily: class I histocompatibility antigen; immunoglobuli
C;Keywords: 91ycoprotein
F;4-90/Region: domain A
F;91-182/Region: domain B
F;1-182/Region: domain B
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Apr-1995 #sequence_revision 26
C;Accession: JX0353
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Best Local
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Best Local
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106,237/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                        Local Si
hes 165;
  4 QDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNSKDRKSQPMGLWRQVEGMEDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKDY IEFNKEIPAWYPFDPAAQITKQKWEAEPYYYQRAKAYLEEECPATLRKYLKYSKNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPRODPPSVVVTSHOAPGEKKKLKCLAYDFYFGKIDVHWTRAGEVQEEELRGDVLHNGNG
                                                          Similarity 60.05; Conservative
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Pred. No. 1.3e-105;
                                                                                Score 901; DB 2;
Pred. No. 3.7e-61;
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C;Species: Mus musculus (house mouse)
C;Date: 22-Apr-1995 #sequence_revision
C;Accession: JX0352; I84729
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A;Title: The MHC class I-like Zn-alpha 2-glycoprotein gene A;Reference number: 149450; MUID:95317827; PMID:7797272
A;Accession: 184729
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A; Residues: 218-287 < RES>
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A;Experimental source: liver
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Best Local
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                                                                                                      FIEFNKEIPAWIPLDPAAANTKLKWEAEKVYVQRAKAYLEEECPEMLKRYLNYSRSHLDR
                                                                                                                                                                               EKESQLQRAREEIFLVTLKDIMDYYKDTTGSHTFQGMFGCEITNNRSSGAVWRYAYDGED
                                                                                                                                                                                                                                                        ETGSYSLTFLYTGLSRPSKGFPRFQATAFLNDQAFFHYNSNSGKAEPVGPWSQVEGMEDW 61
                                                   QDPPSVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGQ--VQEPELRGDVLHNGNGT 239
                                                                                                                                                                                                 KEDSQLQKARED--METLKDIVEYYNDSNGSHVLQGRFGCEIENNRSSGAFWKYYYDGKD 121
                             IDPPTVTITSRVIPGGNRIFKCLAYGFYPQRISLHWNKANKKLAFEPE-RG-VFPNGNGT
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                                                                                                                                                                                                                                                                                                                                   Score 877; DB 2;
Pred. No. 2.6e-59;
6; Mismatches 70
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YQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWE

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C;Superfamily: class I histocompatibility antigen; inmuc;Keywords: duplication; glycoprotein; heterodimer; suf;1-24/Domain: signal sequence #status predicted <SIG>F;25-114/Domain: alpha-1 <EX1>F;115-206/Domain: alpha-2 <EX2>F;115-206/Domain: immunoglobulin homology <IMM>F;220-285/Domain: immunoglobulin homology <IMM>
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A; Residues: 350-362 (RES>
A; Residues: 350-362 (RES>
K; Cross-references: GB:M15634; NID:g187661; PIDN:AAA59615.1; PII
R; Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger,
Immunogenetics 20, 237-252, 1984
A; Title: Inter-locus and intra-allelic polymorphisms of HLA class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Trapani, J.A.; Mickelson, C.A.; Deacon, N.J.; Hooker, D.J.; McKenzie, Immunogenetics 22, 399-405, 1985
A;Title: Molecular cloning and partial nucleotide sequence of a 3.5 kb | A;Reference number: 154420, MUID:86032060; PMID:2997032
A;Accession: 154420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Tragardh, L.; Rask, L.; Wiman, K.; Fohlman, J.; Peterson, P.A. Proc. Natl. Acad. Sci. U.S.A. 77, 1129-1133, 1980
A;Title: Complete amino acid sequence of pooled papain-solubilized A;Reference number: A93840; MUID:80145722; PMID:6928663
A;Accession: A93840
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                                                                                                                                                            F;307-331/Domain: transmembrane #status predicted <TMM>
F;332-362/Domain: intracellular #status predicted <INT>
F;130/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;125-188,227-283/Disulfide bonds: #status experimental
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C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A; Residues: 63-93,'H',95-362 <RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Inter-locus and intra-allelic polymorphisms of A; Reference number: I54412; MUID:84287690; PMID:6332068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 25-265, 'E', 267-295 < ORR>
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C;Date: 31-Jul-1980 #sequence_revision
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ENQDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEG
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113; Conser
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                                                                                  35.0%;
39.9%;
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                                                        Score 527; DB
Pred. No. 1.3e
49; Mismatches
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                                                                                                          DB 1;
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                                                                                     3e-32;
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                                                                                                 C;Species: Homo sapiens (man)
C;Date: 04-Oct-1996 #sequence_revision
C;Accession: 137515
                       C;Accession: I37515
R;Vilches, C.; de Pablo, R.;
Immunogenetics 39, 219, 1994
A;Title: Nucleotide sequence
                                                                                                                                                                                             MHC class I histocompatibility antigen HLA-B*2706 alpha chain
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C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
C;Accession: I59551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Antigens 44, 318-321, 1994
A;Title: Structure of a novel subtype of B7 (B*0705) isolated
A;Reference number: I59651; MUID:95184211; PMID:7878658
A;Accession: I59651
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A; Residues: 1-362 < RES>
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Best Local S
Matches 113
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nes 113; Conserv
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                                      HNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
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                                                                                                    AYDGKDYTALNEDLRSWTAADTAAQITQRKWEAAREAEQR-RAYLEGECVEWLRRYLENG
                                                                                                                                                                                                  YYDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYS
                                                                                                                                                                                                                                                                                   MEDWKEDSQLQK--AREDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKY 115
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PAGDRTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS
                                                                                 KDKLERADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VETR 258
                                                                                                                                                                                                                                                                                                                                                                ENQDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGDRTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS
                                                                                                                                                                                                                                                                                                                          ETWAGSHSMRYFYTSVSRPGRGEPRFISVGYVDDTQFVRFDSDAASPREEPRAPWIEQEG
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Pred. No. 1.3e-32;
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cleotide sequence of HLA-B*2706
number: I37515; MUID:94102824;

PMID:8276469

Kreisler,

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precursor

Tue

Feb

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A;Residues: 1-362 <RES>
A;Cross references: EMBL:X73578; NID:g975658; PIDN: C;Genetics:
A;Gene: GDB:HLA-B
A;Gene: GDB:FLA-B
A;Cross references: GDB:120048; OMIM:142830
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; F;220-285/Domain: immunoglobulin homology <IMM>
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A;Status: preliminary; 1
A;Molecule type: mRNA
A;Residues: 1-362 <RES>
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-34,'A',36-90,'C',92,'TNT',96-120,'W',122-136,'Y',138-139,'F',141-154,'S'
A;Cross:references: GB.M24032; NID:g187816; PIDN:AAA59664.1; PID:g386902
R;Bronson, S.K.; Pei, J.; Taillon-Miller, P.; Chorney, M.J.; Geraghty, D.E.; Chaplin, Proc. Natl. Acad. Sci. U.S.A. 88, 1676-1680, 1991
A;Title: Isolation and characterization of yeast artificial chromosome clones linking.
A;Reference number: I59188; MUID:91156671; PMID:2000377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 02-Uul-1996 #sequence-revision 02-Jul-1996 #text_change
C;Date: 02-Uul-1996 #sequence-revision 02-Jul-1996 #text_change
C;Accession: I61865; I61862; I79639
R;Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
J. Immunol. 142, 3937-3950, 1989
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A;Reference number: I36956; MUID:89235215; PMID:2715640
A;Accession: I61865
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-362 <RES>
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A; Map position: 6p21.3-6p21
A; Introns: 115/1
C; Superfamily: class I histo
C; Keywords: glycoprotein; ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M24034; NID:g187822; PIDN:AAA59667.1; A;Accession: I61862
                                                                           A;Cross-references: GDB:120048; OMIM:142830 A;Map position: 6p21.3-6p21.3
                                                                                                                                                                        A;Residues: 26-34,'A',36-90,'C',92,'TNT',96-120,'W',122-136,'Y',138-139,'F',141-154,'S'
A;Cross-references: GB:M59840; NID:g187758; PIDN:AAA59646.1; PID:g187759
                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                              A; Gene: GDB: HLA-B
                                                                                                                                                      C; Genetics
                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                                                                                                                                                          A; Accession: 179639
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Best Local
       Superfamily: class I histocompatibility antigen; Keywords: glycoprotein; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVL
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110; Conserv
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Pred. No. 1.8e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Homo sapiens (man)
C; Date: 19-Mar-1997 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete nucleotide sequence of HLA-B*0703, a A;Reference number: S60601; MUID:94148707; PMID:8106270 A;Accession: S60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Bergmans, A.M.C.; Tijssen, H.; Lardy, N.; Hum. Immunol. 38, 159-162, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S60601
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A; Residues: 1-362 <BER>
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Best Local
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                                                                                                                                           YYDGKDYIEFNKEIPAWVPFDPAAQITKOKWEAEPVYVQRAKAYLEEECPATLRKYLKYS
                                                                                                                                                                                                                                                                               ENQDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEG
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                                                                                                                         AYDGKDYIALNEDLRSWTAADTAAQITQRKWEAAREAEQR-RAYLEGECVEWLRRYLENG
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                                                            KDKLERADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL~VETR
                                                                                        KNILDRODPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVL 233
                                                                                                                                                                                       PEYWDRNTQIYKTNTQTDRESLRNLRGYYNQSEAGSHTLQSMYGCDVGPDGRLLRGHDQY
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Pred. No. 2.2e-32;
                                                                                                                                                                                                                                                                                                                     Score 522; DB:
Pred. No. 3.1e-
49; Mismatches
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7;

I80169 class I histocompatibility

antigen

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chimpanzee

(fragment)

RESULT

9

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RESULT 10
S18197
class I histocompatibility antigen Gogo-A3 alpha chain - gorilla
G;Species: Gorilla gorilla (gorilla)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
C;Accession: S18197
R;Watkins, D.I.; Chen, Z.W.; Garber, T.L.; Hughes, A.L.; Letvin,
Immunogenetics 34, 185-191, 1991
A;Title: Segmental exchange between MHC class I genes in a highe
A;Reference number: S18197; MUID:91372865; PMID:1894312
A;Accession: S18197
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A, Title: A uniquely high level of recombination at the HLA-B A, Reference number: I59308; MUID:94286544; PMID:8016085
A, Accession: I80169
A, Accession: I80169
                                                                                                                                                                                                                                                                                                                                                        A:Molecule type: nucleic acid
A:Residues: 1-354 <WAT>
A:Residues: 1-354 <WAT>
A:Cross-references: EMBL:X54375; NID:g22889; PIDN:CAA38250.1; PID:g22890
A:Cross-references: EMBL:X54375; NID:g22889; PIDN:CAA38250.1; PID:g22890
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
E;212-277/Domain: immunoglobulin homology <IMM>
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C;Date: 24-May-1996 #sequence_revision
C;Accession: 180169
R;McAddam, S.N.; Boyson, J.E.; Liu, X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-355 < RES>
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                                       ---YDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLK 173
                                                                                   DRNTQIYKAQAQTDRVDLETLRG---YYNQSEGGSHTIQRMYGCEV--~GPDGRFLRGYL 130
                                                                                                              KEDSQLQKA-----REDMETLKDIVEYYNDS-NGSHVLQGRFGCEIENNRSSGAFWKYY- 116
                                                                                                                                                                        GSHSMRYFYTTMSRPGRGEPRFISVGYVDDTQFVRFDSDDASPREEPRAPWMEREGPEYW 76
                                                                                                                                                                                               GRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNSKDR--KSQPMGLWRQVEGMEDW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KETLQRADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VETR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEYWDRETRNMKASAQTDRENLRIALRYYNQSEAGSHIIQRMYGCDMGPDGRLLRGYYQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENQDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEG 59
QDAYDGKDYITLNEDLRSWTAADMAAQITQRKWEAAR-EAERLRAYMEGTCVEWLRRHLE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEGDRTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS 293
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39.3%;
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; Pred. No. 3.6e-32;
48; Mismatches 115
                                                                                                                                                                                                                                                                  46;
                                                                                                                                                                                                                                                                                  Score 519; DB 2
Pred. No. 5e-32;
                                                                                                                                                                                                                                                                                                                                                     homology
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                                                                                                   class I histocompatibility antigen - pygmy chimpanzee (fragment) (;Species: Pan paniscus (pygmy chimpanzee, bonobo) (;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change C;Accession: I80165
                R;MCAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, Proc. Natl. Acad. Sci. U.S.A. 91, 593-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B A;Reference number: I59308; MUID:94286544; PMID:8016085
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#text_change 21-Jan-2000

A.L.;

Bontrop,

R.E.;

Wat

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A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1 C;Superfamily: class I histocompatibility antigen; im C;Keywords: transmembrane protein E;1-24/Domain: signal sequence #status predicted <SIG F;25-362/Product: class I histocompatibility antigen F;25-114/Domain: alpha-1 <ALL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex A;Reference number: JH0534; MUID:92078860; PMID:1744581
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JH0538
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F;207-298/Domain: alpha-3 <AL3>
F;220-285/Domain: immunoglobulii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           class I histocompatibility antigen Gogo-Oko heavy chain precursor -
C:Species: Gorilla gorilla gorilla (lowland gorilla)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-J
C:Accession: JH0538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: EBV-transformed C; Genetics:
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A; Residues: 1-362 <LAW>
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                                                                                                                                                                                                                                                                                         DRNTQIYKAQAQTDRVDLETLRG---YYNQSEGGSHTIQRMYGCEV---GPDGRFLRGYL 138
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                                               VLHNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                 NGKETLQRTDPPKTHMTHHPVSDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VE
                                                                                                                                           YSKNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGD 231
                                                                                                                                                                                                                                                                                                                 GSHSMRYFYTTMSRPGRGEPRFISVGYVDDTQFVRFDSDDASPREEPRAPWMEREGPEYW 84
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TRPGGDGTFQKWAAVVVPSGKEQRYTCHVQHEGLPKPLTLRWEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                 GRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNSKDR--KSQPMGLWRQVEGMEDW 63
                                                                                                                                                                                             QDAYDGKDYITLNEDLRSWTAADMAAQITQRKWEAAR-EAERLRAYMEGTCVEWLRRHLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.5%; Score 519; DB 2; 39.3%; Pred. No. 5.2e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHC class I protein - chimpanzee C:Species: Pan troglodytes (chimpanzee) C:Date: 04-Oct-196 #sequence_revision C:Accession: I36961
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A;Molecule type: mRNA
A;Residues: 1-354 <RES>
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TRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS
                                                                                                                                          KEDSQLQKA-----REDMETLKDIVEYYNDS-NGSHVLQGRFGCEIENNRSSGAFWKYY- 116
                                                                                                                                                                                                                                                                                    GSHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYW
                                                                                                                                                                                                                                                                                                                   GRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEGMEDW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAGDRTFQKWAAVVVPSGQEQRYTCHVQHEGLAEPLTLRWEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YYDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDWKEDSQLQK--AREDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENQDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEG
                                   VLHNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                      NGKETLQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VE
                                                                                                     YSKNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGD
                                                                                                                                                                                                                DEETRSAKAHSQTDRVDLGTLRG---YYNQSEDGSHTIQIMYGCDV---GSDGRFLRGYR
                                                                                                                                                                                                                                                                                                                                                        114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEYWDRNTQICKAQAQTDRESLGNLRGYYNQSEAGSHTLQTMYGCDVGPDGRFLRGYRQF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETWAGSHSMRYFYTSVSRPGRGEPRFISVGYVDDTQFVRFDSDAASPREEPRAPWMEQEG
                                                                                                                                                                           ---YDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLK
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112; Conser
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                                                                                                                                                                                                                                                                                                                                                        46;
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                                                                                                                                                                                                                                                                                                                                                      Score 518; DB 2;
Pred. No. 6.2e-32;
6; Mismatches 103
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7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB/EMBL/DDBJ
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6e-32;
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LEXP. Med. 163, 1173-1190, 1986
A;Title: Secretion of HLA-A and -B antigens via an alternative A;Reference number: I55659; MUID:86198522; PMID:3701253
A;Accession: I55659
                                  A; Title: A novel HLA-B27 allele maps B27 allospecificity A; Reference number: I56116; MUID:91268545; PMID:1711072 A; Accession: I56116
                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: T56116
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A;Map position: 6p21.3-6p21.3
A;Introns: 25/1, 115/1, 207/1; 299/1; 338/1
C;Superfamily: class I histocompatibility antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Little, A.M.; Madrigal, J.A.; Parham, P. Immunogenetics 35, 41-45, 1992 A;Title: Molecular definition of an elusive third HLA-A9 A;Reference number: I54493; MUID:92104637; PMID:1729171 A;Accession: I54493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHC class I histocompatibility antigen HLA-A alpha chain precurs (;Species: Homo sapiens (man) C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change C;Accession: I54493; I55659
A; Status: 1
A; Molecule
                                                                                                          R;Choo, S.Y.; Fan, L.A.; Hansen, J.A. J. Immunol. 147, 174-180, 1991
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A; Cross-references: GB:M12377; NID:g187607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 271-365 < I
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A; Residues: 1-365 < R
                                                                                                                                                                                                                          MHC HLA-B27-HS -
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                    preliminary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSHSMRYFSTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYW
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type: mRNA
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                    translated from GB/EMBL/DDBJ
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Pred. No. 6.2e-32;
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A;Cross-references: GB:M62852; NID:g187760; PIDN:AAA59647.1; PID:g187761
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;196-261/Domain: immunoglobulin homology <IMM>
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                                                        238 GTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS 276
 239
                                                                                                                                                                           | GSHSMRYFHTSVSRPGRGEPRFITVGYVDDTLFVRFDSDAASPREEPRAPWIEQEGPEYW 60
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RTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS 277
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Search completed: February 4, 2003, 10:06:01 Job time : 19 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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          3300887
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Gapop 10.0 , Gapext 0.5
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     SwissProt_40:*
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Sanchez L.M., Chirino A.J., Bjorkman P.J.;
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"Hydrophobic ligand binding by Zn-alpha 2-glycoprotein, a
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TISSUE SPECIFICITY: Blood plasma, seminal plasma, sweat, epithelial cells of various human glands, 1 SIMILARITY: HIGH, TO THE EXTRACELLULAR DOMAIN OF TOF CLASS I MHC ANTIGENS.
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Q65678; Q65523;

Q1-NOV-1997 (Rel. 35, Creat

O1-NOV-1997 (Rel. 35, Last

15-UL-1999 (Rel. 38, Last

Zinc-alpha-2-glycoprotein p

(Zn-alpha-2-GP).
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                                                                                                                                               "CLOULING TO THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAT
                                                                                                                                                                                                                                       TISUE-Liver;
MEDLINE-9433816; PubMed-8056339;
Fueyo A. Uria J.A., Freije J.M.P.,
"Cloning and expression analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Sprague-Dawley; TISSUE-Liver; MEDLINE-95155283; PubMed-7852290; Ueyama H., Naitoh H., Ohkubo I.; "Structure and expression of rat and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
MEDLINE=95155283; PubM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Mammalia; 1
                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE OF 4-296 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYSKNI
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274; Conser
           HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria;
                                 PANCREAS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s (Rat).
oa; Chordata;
ia; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256
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                                   OVARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
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MY -> MWASMSRML (IN REF. 2).

Q -> E (IN REF. 6).

E -> Q (IN REF. 6).

E -> Q (IN REF. 6).

AVPPQDTAPYSCHVQHSSLAQPLVVPWEAS -> QCPRRTQ
PPTPATCSTAAWPSPSGCPGRPARKQGLEAMWDLRPSSCPS
CLMWELNHRNHSQW IHKA (IN REF. 5).

MW; 6C6A7541A2F6371A CRC64;
                                   PROSTATE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         precursor (Zn-alpha-2-glycoprotein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1487; D
Pred. No. 1.5e
2; Mismatches
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                                                                                                                                                                     ED DEGRADATION IN ASSOCIATED WITH
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Sciurognathi;
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                                                               IN LIVER,
E, MAMMARY
                                                                                                                                                                                                                                                                           Lopez-Otin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata;
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                                                               BUT NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muridae;
                                                                                                                                                                          N ADIPOCYTES AND CAUSES SOME ADVANCED CANCERS
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                                                                    KIDNEY,
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; Murinae; Rat
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                                            SPLEEN,
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                                                                    WIDE NUMBER
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DISULFID
CARBOHYD
                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
21nc-alpha-2-glycoprotein precursor (Zn-alpha-2-glycoprotein)
(Zn-alpha-2-GP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outsy the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                       Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00129; MHC_I; 1.
ProDom; PD000050; MHC_I; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D21058; BAA04637.1; -. EMBL; X75309; CAA53057.1; -. HSSP; P25311; 1ZAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  NCBI_TaxID=10090;
                                                 AZGP1
                                                                                                                      Q64726;
                                                                                                                                  ZA2G_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00290; IG_MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                    ODPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGQ--VQEPELRGDVLHNGNGT
                                                                                                                                                                                                         YQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWE
                                                                                                                                                                                                                                                                                                   YIEFNKEIPAMVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYSKNILDR
                                                                                                                                                                                                                                                                                                                                                   QDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNSKDRKSQPMGLWRQVEGMEDW
                                                                                                                                                                                          YLSWMEVEVPPQNRDPFVCHIEHKGLSQSLSVQWD
                                                                                                                                                                                                                                          TDPPTVKITSRVAPGRNRIFRCLAYDFYPQRISLHWNQASKKLASEPE-RG-VFPNGNGT
                                                                                                                                                                                                                                                                                       FIEFNKEIPAWIPLDPAAANTKLKWEAEKVYVQRAKAYLEEECPTMLKKYLTYSRSHLDR
                                                                                                                                                                                                                                                                                                                                      EKESQLQRAREEIFLVTLKDIMDYYEDSTGSHTFQGMFGCEITNNRSSGAVWRYAYDGED
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                                                                                                                                                                                                                                                                                                                                                                                                                                     165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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IPR003600; Ig_like.
IPR001039; MHC_I.
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             Rodentia;
                        Chordata;
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ZINC-ALPHA-2-GLYCODROTEIN.
PYRROLIDONE CARBOXYLIC ACID
SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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OF CHARGE (GLCARC. . .) (POT
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            Craniata; Ver
Sciurognathi;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003600; Ig_like.
InterPro; IPR001039; MHC_I.
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ProDom; PD000050; MHC_I; 1.
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SMOSITE; PS00290; IG_MHC; FALSI
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-i- FUNCTION: STIMULATES LIPID DEGRADATION
THE EXTENSIVE FAT LOSSES ASSOCIATED WIT
SIMILARITY).
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MEDLINE=95155283; PubMed=7852290;
Ueyama H., Naitoh H., Ohkubo I.;
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"Structure and expression of rat and
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BY SIMILARITY.
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Pred. No. 1
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RESULT 4
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SEQUENCE FROM N.A.

MEDLINE-90315860; PubMed-2700944;

Parham P., Benjamin R.J., Chen B.P., Cl

Krensky A.M., Lawlor D.A., Littman D.R.

Salter R.D., Zemmour J.;

"Diversity of class I HLA molecules: fuinteractions with T cells.";

Cold Spring Harb. Symp. Quant. Biol. 54
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MEDLINE=90207291; PubMed=2320591;

MEDLINE=90207291; PubMed=2320591;

Ennis P.D., Zemmour J., Salter R.D., Parham P.;

Ennis P.D., Zemmour J., Parh
                                                                                                                                                                                                                                                                                                                                              Orr H.T., Lopez de Castro J.A., Lancet D., Strominger J.L.; "Complete amino acid sequence of a papain-solubilized human histocompatibility antigen, HLA-B7. 2. Sequence determination search for homologies.";
Biochemistry 18:5711-5720(1979).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Last sequ
16-OCT 2001 (Rel. 40, Last anno
HLA class I histocompatibility
precursor (B7.2).
                  EMBL;
EMBL;
PIR; /
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21-JUL-1986
                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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MEDLINE=80088278; PubMed=518865;
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Eukaryota; Metazoa; (
Mammalia; Eutheria; l
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                  L; M32317; AAA36230.1;
L; M16102; AAA59622.1; Z
L; U29057; AAA91229.1; Z
; A02185; HLHUB7.
                                                                                                                                                                                                                                                                                                          MICROGLOBULIN)
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                                                                                                                              an email to license@isb-sib.ch).
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40, Last annotation update)
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InterPro: IPR003597; Ig_cl.
InterPro: IPR001039; MHC_I.
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Pfam; PF00047; MHC_I: 1.
ProDom; PD000050; MHC_I: 1.
SMART; SM00407; IGcl: 1.
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GL -> RP (IN REF. 3).
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9; Mismatches 111
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B-7 B*0702 ALPHA CHAIN
EXTRACELLULAR ALPHA-1.
                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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EXTRACELLULAR ALPHA-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The nucleotide sequence of HLA-B*2704 reveals substitution in exon 4 which is also present in Immunogenetics 43:160-162(1996).
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InterPro; IPR003597; Ig_c1.
InterPro; IPR001039; MHC_I.
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Vilches C., de Pablo R., Krelsler N
"Nucleotide sequence of HLA-B*2706.
Immunogenetics 39:219-219(1994).
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Mammalia; Eutheria; Primates;
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MHC I; Transmembrane;
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SUBJULT: DIMER OF ALPHA CHAIN AND A BETA C
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                                     MEDWKEDSQL--QKAREDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKY
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Catarrhini; Hominidae
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Query Match
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Pfam; PF00129; MHC_I; 1.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGC1; 1.
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Class I histocompatibility antigen, GOGO-GOC alpha ch
Gorilla gorilla gorilla (Lowland gorilla)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Lawlor D.A., Warren E., Taylor P., Parham P
"Gorilla class I major histocompatibility c
to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-i- FUNCTION: INVOLVED IN THE PRESENTATION
THE IMMUNE SYSTEM.
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PROSITE; PS00290; IG_MHC; 1.
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                       SEQUENCE
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CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-OKO ALPHA CHAIN.

EXTRACELLULAR ALPHA-1.

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MBL outstation -
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Matches 11
                                                                                                           InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR001039; MHC_I.
Pfam; PF00047; ig; l.
Pfam; PF00047; ig; l.
Pfam; PF000029; MHC_I; l.
ProDom; PD000050; MHC_I; l.
SMART; SM00407; IGCl. l.
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01-APR-1990 (Rel. 14,
01-APR-1993 (Rel. 25,
                                                                                                                                                                                                                                    entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                               EMBL; M30678;
HSSP; Q95352;
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Lawlor D.A., Warr
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                                                                                     PROSITE; PS00290; IG_I MHC I; Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                      lor D.A., Warren E., Ward F.E., mparison of class I MHC alleles unol. Rev. 113:147-185(1990). EUNCTION: INVOLVED IN THE PRESE
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SUBUNIT: DIMER OF ALPHA CHAIN AND
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  histocompatibility
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6; Mismatches 105;
            EXTRACELLULAR ALPHA-1
EXTRACELLULAR ALPHA-2
EXTRACELLULAR ALPHA-3
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        InterPro;
InterPro;
InterPro;
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01-APR-1993 (Rel. 25, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
HLA class I histocompatibility antigen, B-27
                                                                                                      modified
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                                                                                                                                                                                                                     position
                                                                                                                                                                                                                                                    MEDLINE-91268545;
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Mammalia; Eutheria;
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P30467;
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                                                                                                                        European
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                                                                                                                                                                                      THE IMMUNE SYSTEM
                                                                                                                                                                                                FUNCTION: INVOLVED IN THE PRESENTATION
                                                                                                                                                                                                       Y.S., Fan L.A., Hansen J.A.;
ovel HLA-B27 allele maps B27 allospecificity
tion 70 in the alpha 1 domain.";
mmunol. 147:174-180(191).
                                                                                                                                                                                                                                                                                                               sapiens (Human)
                                                                                                                      SWISS-PROT entry is copyright. It is produced through
meen the Swiss Institute of Bioinformatics and the EM
European Bioinformatics Institute. There are no restr
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                                        142830;
                                                M62852;
P03989;
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       IPR003006;
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A., Hansen J.A.;
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Catarrhini;
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1B16_HUMAN
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CARBOHYD
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDILINE-88227491; PubMed=3286582;
Choo S.Y., St John T., Orr H.T., Hansen J.A.;
Choo S.Y., St John T. Orr H.T., Hansen J.A.;
"Molecular analysis of the variant alloantigen HLA-
identifies a unique single amino acid substitution.
Hum. Immunol. 21:209-219(1988).

-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FORE:
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor (B-27D).
HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat.
HLA class I histocompatibility antigen, B-2
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ProDom; PD000050; MHC_1
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                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
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SWISS-PROT entry 1...
ween the Swiss Institute of Blu.... The European Bioinformatics Institute. The non-profit institutions as long that the swing of the swing 
                                                                                                                                                              THE IMMUNE SYSTEM.
SUBUNIT: DIMER OF ALPHA CHAIN
                                                                                                                                               MICROGLOBULIN).
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Primates;
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b; Pred. No. 7.8e
48; Mismatches
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ALPHA-3.
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HSSP; P03989
MIM; 142830;
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DISULFID
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01-APR-1993
01-APR-1993
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HLA Class I
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proDom; PD000050; MHC_I; 1.
SMART; SM00407; IGC1; 1.
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MHC I; Transmembrane;
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SEQUENCE FROM N.A.
MEDLINE=88152906; PubMed=3257938;
MEDLINE=88152906; PubMed=88152906; PubMed=88152906; PubMed=88152906; PubMed=88152906; PubMed=88152906; PubMed=88152906; Pub
                                                                                                                          Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                             HLA-B OR HLAB
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109; Conser
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IPR003597;
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(Rel. 25, Last sequence update)
(Rel. 40, Last annotation update)
histocompatibility antigen, BW-47
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Primates;
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MHC_I.
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N-LINKED (GLCNAC.
BY SIMILARITY.
BY SIMILARITY.
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9; Mismatches
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EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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Catarrhini; Hominidae
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.5e-33;
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                                         В.;
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                       HLA-B13
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RESULT 12
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ID 1A24_H
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TA24_HUMAN STANDARD; PRT; 365 AA. p05534; P30448; P30449; Q95355; P01-NOV-1988 (Rel. 09, Created) 01-NOV-1988 (Rel. 09, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) HLA class I histocompatibility antigen, A-24(A-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00290; IG_
MHC I; Transmembrane;
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SMART; SM00407; IGc1; 1.
PROSITE; PS00290; IG_MHC; 1
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MIM; 142830; -.
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-!- FUNCTION: INVOLVED IN THE PR
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InterPro; IPR001039;
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                                                                                                                                                                                                                                                                                     ENQDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEG
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                                                                                                                                                                                    WKYYYDGKDYIEFNKEIPAWVPTDPAAQITKOKWEAEPVYVQRAKAYLEEECPATLRKYL 172
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                                                                                                      ETRPAGDRTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS
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112; Conser
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N-LINKED (GLCNAC.
BY SIMILARITY.
BY SIMILARITY.
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BW-47 B*47
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No. 8.
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MEDLINE-85206128; PubMed-2987115;

N'Guyen C., Sodoyer R., Trucy J., Strachan

"The HLA-AW24 gene: sequence, surroundings

HLA-A2 and HLA-A3 genes.";
                                                                                                                                                                                                                                                Sawanaka K., Akaza
"A new A9 sequence
                                                                                                                                                                                                                                                                                                                    Gao
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92269955; PubMed=1317015;
Belich M.P., Madrigal J.A., Hildebrand W
Williams R.C., Luz R., Petzl-Erler M.L.,
"Unusual HLA-B alleles in two tribes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenetics 21:479-489(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
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HLA-A OR HLAA.
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"An introni
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                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=98007772; 1
                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 357:326-329(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Little A.-M., Madrigal J.A., Parham Molecular definition of an elusive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (A*2402/A*2403).
MEDLINE=92104637; PubMed=1729171;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                        [6]
                                                                                                                                                                                                                                               new A9 sequence HLA-A9HH from
                                                                                                                                                                                                     3:9-14(1996).

THE IMMUNE SYSTEM.

SUBUNIT: DIMER OF ALPHA CF
                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                      MICROGLOBULIN).
POLYMORPHISM: THE FOLLOWING
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                                                                                                                                                                                                                                                                                                                                                                   intronic mutation
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M15497;
M64740;
M64741;
U19733;
U18987;
Z72422;
D83516;
Q95352;
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                                                                                                       non-profit institutions as long and this statement is not removed.
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                                                                                                                                                                                                                                                                                                          (JAN-1995)
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                                                                                     email to license@isb-sib.ch).
                                                                                                                                                                            A*2403
         AAA59611.1; -. AAA59600.1; -. AAA59600.1; -. AAA596051.1; -. AAB60651.1; JOII; CAA96532.1; -. BAA11936.1; -.
                                                                                                                                                                                                                                                         Tokunaga
Akaza T.,
                                                                                                                                                                                                                                                                                                                                                 50:340-346(1997).
                                                                                                                                                                                                                                                                                                                                                                                               PubMed=9349616;
                                                                                                                                                                            AND
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                                                                                            license agreement (See http://www.isb-sib
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                                                                                                                                                                                                                                                                                                                                                                  responsible
                                                                                                                                                                            A*2408
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Tadokoro K., Juji T.,
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                            JOINED
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L., Parham P.
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1814_ ID AC DT DT DT DE GN

P03989;
23-0CT 1986 (Rel. 02, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HIA class I histocompatibility antigen, B-27

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OR HLAB

RESULT 13

HUMAN

B14_HUMAN

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InterPro; IPR001039; MHC_I.
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Pfam; PF00129; MHC_I; 1.
ProDom; PD00050; MHC_I; 1.
SMART; SM00407; IGcl; 1.
PROSITE; PS00290; IG_MHC; 1
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263
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                                                                                                                         KEDSQLQKA--REDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKYYYDG
GTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS
                                    GRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEGMEDW
                                                       DRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVLHNGN
                                                                                                                                                    GSHSMRYFSTSVSRPGRGEPRFTAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYW
                 GTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                         KDYIALKEDLRSWTAADMAAQITKRKWEAAHV-AEQQRAYLEGTCVDGLRRYLENGKETL
                                                                                    KDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYSKNIL
                                                                                                             DEETGKVKAHSQTDRENLRIALRYYNQSEAGSHTLQMMFGCDVGSDGRFLRGYHQYAYDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
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IG_cl.
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H -> Q (IN A*2408).

/FTId=VAR_004355.

E -> G (IN A*2408).
                                                                                                                                                                                                   Score 517; DB 1;
Pred. No. 8.6e-33
                                                                                                                                                                                                                                                                  /FTId=VAR_004358.
DG -> EW (IN A*2403).
/FTId=VAR_004359.
                                                                                                                                                                                                                                                                                                                /FTId=VAR_004356.
G -> R (IN A*2408).
                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC TAIL. N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA CLASS I HISTOCOMPATIBILITY A-24(A-9) ALPHA CHAIN.
                                                                                                                                                                                                                                        REF. 6).
/FTId=VAR_004360
                                                                                                                                                                                                                                                         A -> T
                                                                                                                                                                                                                                                                                            /FTId=VAR_004357.
Q -> W (IN REF. 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR
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301
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Ezquerra A., Bragado R., Vega M.A., Strominger J.L., Woody J.,
Lopez de Castro J.A.;
"Primary structure of papain-solubilized human histocompatibility
antigen HLA-B27.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the EUROPEUM --- use by non-profit institutious as a modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDIJINE-#6149317; PubMed=3485286;
MEDISERS, Riethmueller G., Weiss E., M
"Complete sequence of HLA-B27 CDNA iden
Characterization of structural markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Organization, sequence and expression molecular approach to analyze HLA and (Immunobiology 170:367-380(1985).
                                                                                                                                                                                                                                                                                        Pfam;
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PIR; /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                x-ray Crystallography (2.1 ANGSTROMS)
MEDLINE=92405152; PubMed=1525820;
Madden D.R., Gorga J.C., Strominger J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -C allelic series.";
Proc. Natl. Acad. Sc
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weiss
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                                                                                                          PROSITE; PS00290; IG_I MHC I; Transmembrane;
                                                                                                                                        ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The symmetry of the sym
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between
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Nature 353:321-325(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                InterPro;
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SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANKYLOSING SPONDYLITIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MICROGLOBULIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A25128; HLHUB2.
S07441; S07441.
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PF00129; MHC_I; 1.
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W., Doerner C., Lang M., Riethmueller G.;
squence and expression of the HLA-B27 gene:
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                                                                                                          Glycoprotein; Signal;
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HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, . B-27 ALPHA CHAIN.
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A identified
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                                   AYDGKDYIALNEDLSSWTAADTAAQITQRKWEAARV-AEQLRAYLEGECVEWLRRYLENG
                                                          YYDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYS
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-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FUTTHE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-86138405; PubMed=3912316; Weiss E.H., Kuon W., Doerner C., Lang M., Riethmueller G.: "Organization, sequence and expression of the HLA-B27 gene: molecular approach to analyze HLA and disease associations. Immunobiology 170:367-380(1985).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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IPR003597;
IPR001039;
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         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
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01-JAN-1990 (Rel. 13, Last seque
01-JAN-1990 (Rel. 13, Last annot
BOLA class I histocompatibility
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Ennis P.D., Jackson A.P., Parham P.;
"Molecular cloning of bovine class I
J. Immunol. 141:642-651(1988).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=88258075;
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P13753;
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                                                                  EMBL
                                                                    a collaboration -
MBL outstation -
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Best Local Similarity
Matches 111; Conserv
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InterPro; IPR003597; Ig_c1.
InterPro; IPR0013597; Ig_c1.
InterPro; IPR001039; MHC_I.
Pfam; PF00047; Ig; 1.
Pfam; PF00129; MHC_I; 1.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IG_MHC; 1.
SMART; SM00407; IG_MHC; 1.
MHC I; Transmembrane; Glycopro
SIGNAL 1
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DISULFID
DISULFID
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ilarity 39.1%;
Conservative '
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                          2003, 10:04:56
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SIGNIFICANT WITH IMMUNOGLOBULIN C-REGION
DOMAINS AND BETA-2-MICROCLOBULIN.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 515; DB 1; Length 364
Pred. No. 1.2e-32;
9; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BL3-7.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   622056CF7DCF7873 CRC64;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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        SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_vertebrate:
13: sp_vertebrate:
14: sp_unclassifie
15: sp_bacteriap:*
16: sp_bacteriap:*
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Gapop 10.0 , Gapext 0.5
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sp_manmal:*
sp_mhc:*
sp_mhc:*
sp_phage:*
sp_phage:*
sp_plant:*
sp_virus:*
sp_virus:*
sp_virus:*
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sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	1	Result
520	521	521	522	522	522	523	523	523	523	526	526	527	527	527	871	Score
34.6	34.6	34.6	34.7	34.7	34.7	34.8	34.8	34.8	34.8	35.0	35.0	35.0	35.0	35.0	57.9	Query Match
357	355	355	362	362	357	362	362	362	356	362	362	362	362	336	307	Length DB
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Q30895 pithecia pi		Q9mxj8 pan troglod	Q29861 homo sapien	Q29638 homo sapien	Q30894 pithecia pi	Q9mxk4 pan troglod	Q29681 homo sapien	Q9mxk1 pan troglod	Q30221 ateles belz	P79489 homo sapien	Q9tp95 homo sapien	Q31613 homo sapien	' Q29854 homo sapien	019782 homo sapien	Q9dbb7 mus musculu	Description

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ALIGNMENTS

MGD; MGI:103163;

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Best Local S
Matches 162
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Interpro; IPR00139; MHC_I.
Pfam; PP00129; MHC_I; 1.
PFAM; PP001638; MHC_I; 1.
PRINTS; PR01638; MHCLLASSI.
PRODOM; PD000050; MHC_I; 1.
SMART; SM00410; IG_like; 1.
SEQUENCE 307 AA; 35332 MW;
                                                                                                                              EMBL;
                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=90207291; PubMed=2320591;

Ennis P.D., Zemmour J., Salter R.D., Parham P.;

Ennis P.D., Zemmour J., Salter R.D., Parham P.;

Ennis P.D., Zemmour J., Salter R.D., Parham P.;

"Rapid cloning of HLA-A,B cDNA by using the polymerase chain frequency and nature of errors produced in amplification.";

Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
         PROSITE;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Rebmann V., Blasczyk
Submitted (JUN-1997)
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Mammalia; Eutheria;
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                     SMART; SM00407;
                                PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC_I; 1.
                                                            Pfam; PF00047; ig; Pfam; PF00129; MHC_
                                                                                                                                                                    IMMUNE SYSTEM (BY SIMILARITY).
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                         HLA-B protein
HLA-B.
                                                                                                                InterPro;
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                                                                                                    InterPro;
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                                                                                                                          MICROGLOBULIN) (BY SIL; Y13567; CAA73901.1; P; P30460; 1AGD.
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162; Conserv
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IPR003006; Ig_MHC
IPR001039; MHC_I.
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                        IGc1;
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Primates;
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58.9%;
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to the EMBL/GenBank/DDBJ
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21,
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Pred. No. 2.8e
36; Mismatches
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                                                                                                                                                                    A BETA CHAIN (BETA-2-
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Matches 113;
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Best Local
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                                                              InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.I.
InterPro; IPR001039; MHC_I.
Pfam; PF00047; Ig; 1.
PFANT; PF00129; MHC_I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; 1.
Glycoprotein; Signal; Transmen SIGNAL.

1 24
FESTINAL.
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Q29854;
Q1-NOV-1996
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01-JUN-2002
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-96369317; PubMed-8773323;

MEDLINE-96369317; PubMed-8773323;

Sanz L., Vilches C., de Pablo R., Bunce M., Moreno M.E., Kreisler "Haplotypic association of two new HLA class I alleles: Cw*15052 a 8*0706: evolutionary relationships of HLA- Cw*15 alleles.";

Tissue Antigens 47:329-332(1996).

-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                              HLA-B alpha chain antigen HLA-B7_L79.
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                       IMMUNE SYSTEM (BY SIMILARITY).
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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L; X91749; CAA62864.1; -.
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113; Conserv
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               Similarity
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38086 MW;
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Primates;
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39.9%;
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01, Last sequence update)
21, Last annotation updat
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Pred. No. 1.7e-37;
9; Mismatches 11:
                                                      POTENTIAL.
; D2D0B3728FFCCD5A CRC64;
 Score 527; DB 7;
pred. No. 1.9e-37;
9; Mismatches 111
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Best Local Similarity
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01-NOV-1996
01-JUN-2002
MHC class I
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Q31613;
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SMART; SM00407; IGc1; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1.
Pfam; PF00129; MHC_I; 1.
PRINTS; PR01638; MHCCLASSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Antigens 44:318-321(1994).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS IMMUNE SYSTEM (BY SIMILARITY).
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-95184211; PubMed=7878658;
Arnett K.L., Adams E.J., Domena J.D.,
"Structure of a novel subtype of B7 (I
individual.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=96128250; PubMed-8537119;

MITH K.D., Epperson D.F., Lutz C.T.;

Smith K.D., Epperson D.F., Lutz C.T.;

"Alloreactive cytotoxic T-lymphocyte-defined peptide antigen presentation.";

Immunogenetics 43:27-37(1996).
                                                                                                                                                                                                                                                                                                               InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001039; MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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L; U21052; AAA92563.1; -.
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P30460; LAGD.
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antigen heavy chain precursor.
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40473
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                       Score 527; DB 7;
Pred. No. 1.9e-37;
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01-MAY-2000
01-JUN-2002
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ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGC1; 1.
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Submitted (SEP-1999) t
                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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InterPro; IPR001039; MHC
Pfam; PF00047; ig; 1.
Pfam; PF00129; MHC_I; 1.
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-1- SUBUNIT: DIMER OF ALPHA CHAIN AND MICROGLOBULIN) (BY SIMILARITY).
EMBL; AF189017; AAF101052.1; -
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Mammalia; Eutheria;
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Marincola F.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                          116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176
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                        YYDGKDYIBENKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYS
AYDGKDYIALNEDLRSWTAADTAAQITQRKWEAAREAEQR-RAYLEGECVEWLRRYLENG
                                                                                                         MEDWKEDSQLQK--AREDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKY
                                                                                                                                                                                         ENQDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAGDRTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEYWDRNTQIYKAQAQTDRESLRNLRGYYNQSEAGSHIIQRMYGCDVGPDGRLLRGHDQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYDGKDYIALNEDLRSWTAADTAAQITQRKWEAAREAEQR-RAYLEGECVEWLRRYLENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDWKEDSQLQK--AREDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKY
                                                                                                                                                                       ETWAGSHSMRYFYTSVSRPGRGEPRFISVGYVDDTQFVRFDSDAASPREEPRAPWIEQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEYWDRNTQIYKAQAQTDRESLRNLRGYYNQSEAGSHTLQSMYGCDVGPDGRLLRGHNQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENQDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDKLERADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETWAGSHSMRYFYTSVSRPGRGEPRFISVGYVDDTQFVRFDSDAASPREEPRAPWIEQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P30460; 1AGD
                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                               362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .P.,
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                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hadzikadic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                             40541 MW;
                                                                                                                                                                                                                                                                            35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig_cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13,
13,
21,
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HE PRESENTATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence up
Last annotation
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                                                                                                                                                                                                                                                        Pred. No. 2.4
                                                                                                                                                                                                                                                                            Score 526; DB 7; Pred. No. 2.4e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                             92AA0CC3DCDC2747 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dhillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              À
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                                                                                                                                                                                                Length 362
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                                                                                                                                                                                                                                                        Indels
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; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTIGENS
                                                                                                                                                                                                                                                        10;
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RESULT
P79489
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                  Qγ
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 밁
                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 112
                                                                                                                                                                                                                                                                                                                                                                                             "FIVE HLA-B22 group alleles in Japanese.";
Tissue Antigens 0:0-0(1997).

-i- FUNCTION: INVOLVED IN THE PRESENTATION OF
IMMUNE SYSTEM (BY SIMILARITY).

-i- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA OF
MICROGLOBULIN) (BY SIMILARITY).

EMBL; D85761; BAA12868.1; -.

EMBL; D85761; BAA12868.1; -.

HSSP; P30460; 1AGD.
InterPro; IPR003096; Ig_MHC.
InterPro; IPR003096; Ig_MHC.
InterPro; IPR001099; MHC_I.
                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
Pfam; PF00129; MHC_I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGc1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HILA-B*5504.
HOmo sapiens (Human).
Homo sapiens (Human).
Metazoa; Chordata;
Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997 (TrEMBLrel.
01-MAY-1997 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P79489;
P79489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bannai M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                              Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
                                                                                                                                                                                                                                                                                                                       ROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259
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 259
                        234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDKLERADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VETR 258
PAGDRTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS
                HNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                               AYDGKDY TALNEDLRSWTAADTAAQITQRKWEAARV-AEQLRAYLEGTCVEWLRRYLENG
                                                                                                               YYDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYS
                                                                                                                                                  PEYWDRNTQIYKAQAQTDRESLRNLRGYYNQSEAGSHTLQSMYGCDVGPDGRLLRGHNQY
                                                                                                                                                               MEDWKEDSQLQK--AREDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKY
                                                                                                                                                                                                 ETWAGSHSMRYFYTAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPREEPRAPWIEQEG
                                                                                                                                                                                                             ENQDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVL
                                                 KETLQRADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VETR
                                                                        KNILDRODPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVL
                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tokunaga K.,
                                                                                                                                                                                                                                                                                                 n; Transmembrane.
362 AA; 40484 MW;
                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.A.
                                                                                                                                                                                                                                                            39.6%;
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03,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tanaka
                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence
Last anno
                                                                                                                                                                                                                                                Score 526; DB 7;
Pred. No. 2.4e-37;
8; Mismatches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H., Kashiwase
                                                                                                                                                                                                                                                                                                  2FEE2B98C0B5F5BF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence u
annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A BETA CHAIN (BETA-2
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on update)
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                                                                                                                                                                                                                                                                       Length 362;
                                                                                                                                                                                                                                                                                                  CRC64;
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 301
                        276
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tokunaga
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                                                                                                                                                                                                                                                Gaps
                                                                                                                                                  140
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                                                  258
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RESULT 7
Q30221
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Q9MXK1
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Best Local S
Matches 113
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InterPro; IPR003006; Ig_MHC_I
InterPro; IPR001039; MHC_I.
InterPro; IPR001039; MHC_I.
Pfam; PF00047; Ig; 1.
Pfam; PF00129; MHC_I; 1.
PF0D0m; PF001638; MHCCLASSI.
Pr0Dom; PF001050; MHC_I; 1.
SMART; SM00407; IGcl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q30221
Q30221;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2002
Q9MXK1;
01-OCT-2000
01-OCT-2000
01-JUN-2002
MHC class I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Evolutionary instability of the major hist class I loci in new world primates."; Proc. Natl. Acad. Sci. U.S.A. 94:14536-1454-1-1-FUNCTION: INVOLVED IN THE PRESENTATION
                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=980707
Cadavid L.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ateles belzebuth (Long-haired spider monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATBE-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TIEMBLrel. 01, Created)
01-NOV-1996 (TIEMBLrel. 01, Last sequence update)
01-UNV-2002 (TIEMBLrel. 21, Last annotation update)
MHC class I Atbe-B*01 (Fragment).
                                                           Q9MXK1
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U59648; AAB97491.1; -. HSSP; O19673; 1HSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                    246
                                                                                                                                           228
                                                                                                                                                                  186
                                                                                                                                                                                        170
                                                                                                                                                                                                                 127
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                                                                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMUNE SYSTEM (BY SIMILARITY).
SUBUNIT: DIMER OF ALPHA CHAIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MICROGLOBULIN)
                                                                                                                                                                                                                                                            ENQDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNSKDR--KSQPMGLWRQVEG 59
                                                                                                                                LRGDVLHNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                             KYY----YDGKDYIEFNKEIPAWVPEDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLR 169
                                                                                                                                                                                                                                                                                                             GTRAGSHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAAIPRMEPRALMMEQEG
                                                                                                                     L-VETRPAGDGTFQKWAAVVVPSGEEQRYTCYVQHEGLPEPLTLRWEPS
                                                                                                                                                                              KYLKYSKNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPE 227
                                                                                                                                                                  RYLENGKETLQRADPPKTHVTHHPVSDHEATLRCWALGFYPTEITLTWQRDGEDQTQDTE
                                                                                                                                                                                                                RGYRQDAYDGKDYIALNEDLRSWTAADMAAQNTKRKWEAANV-AEQLRAYLEGKCQESLR
                                                                                                                                                                                                                                                                                                                                                         al Similarity
113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              PS00290; IG_MHC; UNKNOWN_1.
tein; Transmembrane.
(TrEMBLrel.)
(TrEMBLrel.)
(TrEMBLrel.)
(TrEMBLrel.)
(antigen.
                                                                                                                                                                                                                                                                                                                                                                                                        356 AA; 39667 MW;
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                           PRELIMINARY;
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787; PubMed=9405648;
Shufflebotham C., Ruiz F.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                          34.8%; Score 523; DI
39.1%; Pred. No. 4.20
tive 50; Mismatches
            15,
15,
21,
           Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94:14536-14541(1997)
                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                         9011AB221B79191B CRC64;
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            update)
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Best Local
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                                                                                                                       Q29681
Q29681;
01-NOV-1996
01-NOV-1996
01-JUN-2002
MHC class I
HLA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Major histocompatibility complex class I d chimpanzee population: implications for HIV Immunogenetics 51:398-409(2000).

-!- EUNCTION: INVOLVED IN THE PRESENTATION IMMUNE SYSTEM (BY SIMILARITY).

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BET MICROGLOBULIN) (BY SIMILARITY).
                                                                      Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000050; MHC_I; 1. SMART; SM00407; IGC1; 1. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
   MEDLINE-96128250;
                      SEQUENCE
                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; SEQUENCE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01638; MHCCLASSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; Pfam; PF00129; MHC_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001039; MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF168410; AAF72791.1; HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              de Groot N.G., Otting N., A Madrigal J.A., Bontrop R.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20322475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                      PAGDRTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS
                                                                                                                                                                                                                                                                                                                                          HNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                          KETLQRADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VETR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AYDGKDYIALNKDLSSWTAADTAAQITQRKWEAARV-AEQLRAYLEGTCVEWLRRYLENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEYMDRNTQGIKTQAQTDRENLRTLLRYYNQSEAGSHTLQSMYGCDMGPDGRLLRGYDQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDWKEDSQ--LQKAREDMETIKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENQDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNSKDR--KSQPMGLWRQVEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YYDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETWAGSQSMRYFYTAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAAIPRMEPRAPWIEQEG
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112; Conserv
                  FROM N.A
                                                                                                                                      96 (TREMBLrel. 01, Created)
96 (TREMBLrel. 01, Last sequence update)
02 (TREMBLrel. 21, Last annotation updat
I antigen heavy chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362
                                                                                                                                                                                                                                  PRELIMINARY;
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2 AA; 40442 MW;
   PubMed-8537119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
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Pred. No. 4.3e-37;
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                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                  362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I diversity in HIV research.";
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                                                                       Hominidae;
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                                                                                                                                                           update)
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                                                                                        Euteleostomi;
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Best Local Similarity Matches 112; Conserv
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Best Local
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Pfam; PF00129; MHC_I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGcl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MICROGLOBULIN) (BY SIMILARITY).

EMBL; U21053; AAA92564.1; -.

HSSP; P30460; 1AGD.

InterPro; IPR003597; Ig_cl.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR001039; MHC_I.

Dfam. DFONOA7. -: -. -.
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-i- FUNCTION: INVOLVED IN THE PRESENTATION OF IMMUNE SYSTEM (BY SIMILARITY).

-i- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA MICROGLOBULIN) (BY SIMILARITY).
"Major histocompatibility complex class chimpanzee population: implications for Immunogenetics 51:398-409(2000).
                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21,
                                                  de Groot N.G., Otting N., Ar Madrigal J.A., Bontrop R.E.;
                                                                                                                                                                        Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                         MHC class I antigen (Lymphocyte antigen). PATR-B OR PATR-B17.
                                                                                                                                                                                                                                                                                                                                 Q9MXK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein;
SIGNAL
                                                                                      MEDLINE=20322475; PubMed=10866106;
                                                                                                          TISSUE-BLOOD;
                                                                                                                        SEQUENCE
                                                                                                                                                       NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                              Q9MXK4;
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                                                                                                                                                                                                                                                                                                                                                                                                                    PAGDRTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDWKEDSQLQK--AREDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENQDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDKLERADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYDGKDYIALNEDLRSWTAADTAAQITQRKWEAAREAEQR-RAYLEGECVEWLRRYLENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YYDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEYWDRNTQIYKTNTQTDRESLRNLRGYYNQSEAGSHTLQSMYGCDVGPDGRLLRGHDQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETWAGSHSMRYFYTSVSRPGRGEPRFISVGYVDDTQFVRFDSDAASPREEPRAPWIEQEG
                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 AA;
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40506 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.8%;
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                                                                  Arguello
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                                                                                                                                                                                                           Last sequence up
                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 523; DB 7; 1
Pred. No. 4.3e-37;
9; Mismatches 112;
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                                                                                                                                                                        Craniata; V
Catarrhini;
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                                                                    Watkins
                 I diversity
HIV research
                                                                                                                                                                                         Vertebrata;
                                                                                                                                                                                                                                                           on update)
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                                                                                                                                                                          Hominidae;
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                 research
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                                                                    D.I.,
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                       h.in
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                                                                                                                                                                                         Euteleostomi;
                                                                      Doxiadis
                                  þ
                                     West
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FROM

N.A

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RESULT 11
Q30894
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Best Loc
Matches
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR001039; MHC_I.
Pfam; PP00047; ig; 1.
Pfam; PP00129; MHC_I; 1.
Pfam; PP00129; MHC_I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGG1; 1.
                                                                                                                                                               01-NOV-1996
01-NOV-1996
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS002
Glycoprotein;
SEQUENCE 362
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Walker C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: INVOLVED IN THE PRESENTATION IMMUNE SYSTEM (BY SIMILARITY).
-i- SUBUNIT: DIMER OF ALPHA CHAIN AND A BET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chimpanzees.";
J. Exp. Med. 183:1761-1775(1996).
                                       SEQUENCE FROM N.A.
MEDLINE=98070787; PubMed=9405648;
Cadavid L.F., Shufflebotham C., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virus epitopes to CD8+
                                                                                                                                                                                                            Q30894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Patr-A and B, the orthologues of
virus epitopes to CD8+ cytotoxic '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96261676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CHIMPANZEE
        class
                            Cadavid L.F., Watkins D.I.;
                                                                                               Pithecia
                                                                                                                    Eukaryota;
                                                                                                                                 Pithecia
                                                                                                                                            PIPI-G
                                                                                                                                                                                                030894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L47297; AAL34346.1; HSSP; P30460; LAGD.
                                                                                   NCBI_TaxID=43777;
                                                                                                          Mammalia; Eutheria;
                  "Evolutionary
                                                                                                                                                                                                                                                                                        234
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                                                                                                                                                      class I
                                                                                                                                                                                                                                                                  PAGDRTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS
                                                                                                                                                                                                                                                                            HNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                             KETLQRADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VETR
                                                                                                                                                                                                                                                                                                                                                        AYDGKDYIALNQDLSSWTAADTAAQITQRKWEAARVAEQR-RAYLEGTCVEWLRRYLENG
                                                                                                                                                                                                                                                                                                                                                                    YYDGKDYIEFNKEIPAWVPFDPAAQITXQKWEAEPVYVQRAKAYLEEECPATLRKYLKYS
                                                                                                                                                                                                                                                                                                                                                                                                  PEYWDRNTQIYKAQAQTDRVSLGNLRGYYNQSEAGSHTLQSMYGCDVGPDGRLLRGYEQY
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                                                                                                                                                                                                                                                                                                                                  KNILDRODPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG---QVQEPELRGDVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00290; IG_MHC; 1.
tein; Transmembrane.
362 AA; 40229 MW;
                                                                                                                                pithecia
                                                                                                                    Metazoa;
                                                                                                                                                    (TrEMBLrel. 01, Create
(TrEMBLrel. 01, Last s
(TrEMBLrel. 21, Last a
pipi-G*01 (Fragment).
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                                                                                                                                                                                                             PRELIMINARY;
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        in
                   instability
                                                                                                                                 (White-faced
                                                                                                          Chordata; Craniata; Ve. Primates; Platyrrhini;
        world
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.8%;
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      of the maprimates.
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                                                                                                                                                                Last sequence up
                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 523; DB 7; 1
Pred. No. 4.3e-37;
7; Mismatches 114;
                   the major
                                                                                                                                                                                                             PRT;
                                                                                                                                 saki)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2B6242FA3A49446A CRC64;
                                         Ruiz F.J.,
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                    histocompatibility complex
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                                                                                                           Vertebrata;
ni; Cebidae;
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                                                                                                           Euteleostomi;
Pitheciinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTIGENS
                                          Hughes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                          A.L.,
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RESULT
Q29638
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Best Loc
Matches
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Pfam; PF00129; MHC_I; 1.
Pfam; PF00129; MHC_I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC_I; 1.
SMART; SN00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                       Q29638;
Q29638;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2002
                                                                                                                                                                                                          Class
HLA-B.
Domena J.D.;

Submitted (DEC-1993) to the EMBL/GenBank/DDBJ-
-I- FUNCTION: INVOLVED IN THE PRESENTATION OF IMMUNE SYSTEM (BY SIMILARITY).

-I- SUBBUNIT: DIMER OF ALPHA CHAIN AND A BETA (
MICROGLOBULIN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U59651; AAB97494.1; -. HSSP; Q59535; 1HHK.
                                                                                                                                                                                    Eukaryota;
Mammalia; E
                                                                                   Tissue
[2]
                                                                                            SEQUENCE FROM N.A.

MEDLINE-95381233; PubMed-7652739;

KUDDANS B.S., Arnett K.L., Adams E.J., Parham

"Definition of a new HLA-B7 subtype (B*0704)

family studies and DNA sequence analysis.";

Tissue Antigens 45:322-327(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR003597; Ig_c1.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR001039; MHC_I.
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                                                                                                                                                                        NCBI_TaxID=9606;
                                                                          SEQUENCE
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nes 112; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OC. NATL. ACAD. SCI. U.S.A. 94:14536-14541(1997).

FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS IMMUNE SYSTEM (BY SIMILARITY).

SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                        KYSKNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRG
                                                                                                                                                                                                                                                                                                                                                                                                                                              WKYYYDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENQDGRYSLTYITTGLSKHVEDVPAFQALGSLNDLQFFRYNSKDR--KSQPMGLWRQVEG
                                                                                                                                                                                                                                                                                                                                                            DVLHNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                 PEYWEEQTRRAKAHAQTFRVNLRTLRG---YYNQSEAGSHTVQTMFGCDLGPDGLFLSGY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETWAGSHSLRYFETSVSRPGRGEPRFTAVGYVDDTQFVRFDSDAAIPRMEPQAAWMEQEG
                                                                                                                                                                                                                                                                                                                                                                                                                             EQYAYDGKDYIALNEDLRSWTAADTAAQITKRKWEAAN-EAERTRAYLESECPEWLHRYL
                                                                         FROM
                                                                                                                                                                                    ; Metazoa;
Eutheria;
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                                                                                                                                                                                                                               antigen
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                                                                          N.A.
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                                                                                                                                                                                     Chordata;
Primates;
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Last annotation updat
                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 522; DB 7; 1
Pred. No. 5.1e-37;
6; Mismatches 112;
                                                                                                                                                                                     Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6E74030925418683 CRC64;
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                                                                                                                                                                                      Hominidae;
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                      CHAIN
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                      (BETA-2
                                                                                                                                                                                                 Euteleostomi;
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                                            ANTIGENS
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RESULT 13
Q29861
ID Q2986
AC Q2986
DT 01-WC
DT 01-WC
DT 01-WC
DT 01-WC
DT WAA-B
OC EUKAZ
OC MAMMMA
OX NCBL;
RN [1]
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RN MEDUL;
RA BETGIN
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Pfam; PF00129; MHC_I; 1.
Pfam; PF00129; MHCCLASSI.
PF0D00059; MHCCLASSI.
PF0D00059; MHCCL; 1.
SMART; SM00407; IGcl; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                 Pfam; PF00047; 19; 1.
Pfam; PF00129; MHC_I; 1.
PRINTS; PR01638; MHCCLASSI.
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94148707; PubMed=8106270; Bergmans A., Tijssen H., Lardy J., Reekers P.; Bergmans A., Tijssen H., Lardy J., Reekers P.; "Complete nucleotide sequence of HLA-B*0703, a B7-variant (BPOT Hum. Immunol. 38:159-162(1993).

-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                    EMBL; X64454; CAA45785.1; -. HSSP; P30460; 1AGD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q29861;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q29861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001039; MHC_I.
Glycoprotein;
                                 PROSITE;
                                                      ProDom; PD00005(
SMART; SM00407;
                                                                                                                                                                          InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR001039; MHC_I.
                                                                                                                                                                                                                                                                                                        IMMUNE SYSTEM (BY SIMILARITY).
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND MICROGLOBULIN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLA-BPOT (classI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAGDRTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \verb+KDKLERADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYDGKDYIALNEDLRSWTAADTAAQITQRKWEAAR-EAEQDRAYLEGECVEWLRRYLENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YYDGKDYIEFNKEIPÄWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEYMDRNTQIYKAQAQTDRESLRNLRGYYNQSEAGSHTLQSMYGCDVGPDGRLLRGHDQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDWKEDSQLQK--AREDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETWAGSHSMRYFYTSVSRPGRGEPRFISVGYVDDTQFVRFDSDAASPREEPRAPWIEQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U04245; AAA87398.1; -. P30460; LAGD.
                                                   PD000050; MHC_I; 1.
SM00407; IGc1; 1.
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                                 PS00290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in; Transmembrane.
362 AA; 40419 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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       Transmembrane
                              IG_MHC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 522; DB 7;
Pred. No. 5.2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06E4D36803020D2D CRC64;
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                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                            B7-variant (BPOT).";
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                                                                                                                                                                                                                                                                                                                               (BETA-2
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; Homo.
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RESULT 14
Q9MXJ8
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 Query Match
Best Local S
Matches 110
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                                                                                       Pfam; PF00047; ig; 1.
Pfam; PF00129; MHC_I; 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                      de Groot N.G., Otting N., Arguello R., Watkins Madrigal J.A., Bontrop R.E.;
"Major histocompatibility complex class I dive chimpanzee population: implications for HIV re Immunogenetics 51:398-409(2000).
--- FUNCTION: INVOLVED IN THE PRESENTATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                   InterPro; IPR003597; Ig_c1
InterPro; IPR003006; Ig_MHC
InterPro; IPR001039; MHC_I
                                                                                                                                                                                                          EMBL; AF168414; AAF72795.1; HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                  IMMUNE SYSTEM (BY SIMILARITY).
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND MICROGLOBULIN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHC class I antigen (Fragment).
                                                     SEQUENCE
                                                              Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20322475; PubMed=10866106;
                                                                                                                                                                                                                                                                                                                                                                  TISSUE-BLOOD;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATR-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9MXJ8;
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 Local Similarity
nes 110; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 PEYWDRNTQIYKTNTQTDRESLRNLRGYYNQSEAGSHTLQSMYGCDVGPDGRLLRGHDQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDWKEDSQLQK--AREDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENQDGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AYDGKDYIALNEDLRSWTAADTAAQITQRKWEAAREAEQR-RAYLEGECVEWLRRYLENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YYDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDKLERADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VETR
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112; Conser
                                                    355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                  39772 MW;
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                                                                                                                                                                               Ig_c1.
Ig_MHC.
             34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
  48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation
 Score 521; DB
Pred. No. 6.2e
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 522; DB 7;
Pred. No. 5.2e-37;
9; Mismatches 112
                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                    F474A2C3EEDC398A CRC64;
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                                                                                                                                                                                                                                                                                                                                        Watkins
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HIV research
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             DB 7;
.2e-37;
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                                                                                                                                                                                                                                                                                                 iversity in a
research.";
                                                                                                                                                                                                                                                                          FOREIGN ANTIGENS
                                                                                                                                                                                                                                                                                                                                      D.I.,
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                        Length 355;
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  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
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                                                                                                                                                                                                                                                                                                                West
  10;
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Gaps
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N

ENQDGRYSLTYTYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEG

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RESULT 15
Q95529
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Best Local S
Matches 110
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Bontrop R.E., Watkins D.I.;
"A uniquely high level of recombination at the HLA-B locus.";
Proc. Natl. Acad. Sci. U.S.A. 91:8893-5897(1994).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
IMMUNE SYSTEM (BY SIMILARITY).
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U05580; AAA50183.1; -. HSSP; P03989; 1HSA. Interpro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-TUN-2002 (TrEMBLrel. 21, Last annotation update)
Class I histocompatibility antigen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1. Pfam; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-TEPPIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q95529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94286544; PubMed=8016085; McAdam S.N., Boyson J.E., Liu X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
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           YYDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYS 175
                                                                                                                                                                                                            ENODGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNS--KDRKSQPMGLWRQVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KETLQRADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VETR 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDWKEDSQLQK--AREDMETLKDIVEYYNDSN-GSHVLQGRFGCEI-ENNRSSGAFWKY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEYWDRETRNMKASAQTDRENLRIALRYYNQSEAGSHIIQRMYGCDMGPDGRLLRGYYQY
                                                                                                      MEDWKEDSQLOK--AREDMETLKDIVEYYNDSN-GSHVLOGRFGCEI-ENNRSSGAFWKY 115
                                                                                                                                                                                ETWAGSHSMRYFYTSVSRPGRGEPRFITVGYVDDTQFVRFDSDAASPRMEPRAPWIEQEG
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                                                                                                                                                                                                                                                                                                                   Similarity
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IPR003006; Ig_MHC.
IPR001039; MHC_I.
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                                                                                                                                                                                                                                                                                         34.6%; Score 521; DB 7; ilarity 38.9%; Pred. No. 6.2e-37; Conservative 48; Mismatches 115
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251
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                                             KETLQRADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTEL-VETR
                                                           KNILDRQDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAG--QVQEPELRGDVL
                      HNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEAS
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